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(54) Title: NEUROTRANSMISSION-ASSOCIATED PROTEINS

(57) Abstract: Various embodiments of the invention provide human neurotransmission-associated proteins (NTRAN) and polynucleotides which identify and encode NTRAN. Embodiments of the invention also provide expression vectors, host cells, antibodies, agonists, and antagonists. Other embodiments provide methods for diagnosing, treating, or preventing disorders associated with aberrant expression of NTRAN.



WO 03/051902 A1



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NEUROTRANSMISSION-ASSOCIATED PROTEINS

TECHNICAL FIELD

The invention relates to novel nucleic acids, neurotransmission-associated proteins encoded by these nucleic acids, and to the use of these nucleic acids and proteins in the diagnosis, treatment, and prevention of autoimmune/inflammatory, cardiovascular, neurological, developmental, cell proliferative, transport, psychiatric, metabolic, and endocrine disorders. The invention also relates to the assessment of the effects of exogenous compounds on the expression of nucleic acids and neurotransmission-associated proteins.

10

BACKGROUND OF THE INVENTION

The human nervous system, which regulates all bodily functions, is composed of the central nervous system (CNS), consisting of the brain and spinal cord, and the peripheral nervous system (PNS), consisting of afferent neural pathways for conducting nerve impulses from sensory organs to the CNS, and efferent neural pathways for conducting motor impulses from the CNS to effector organs. The PNS can be further divided into the somatic nervous system, which regulates voluntary motor activity such as for skeletal muscle, and the autonomic nervous system, which regulates involuntary motor activity for internal organs such as the heart, lungs, and viscera. CNS-associated proteins function in neuronal signaling, cell adhesion, nerve regeneration, axon guidance, neurogenesis, and other processes.

The cerebral cortex or higher brain is the largest structure, consisting of a right and a left hemisphere interconnected by the corpus callosum. The cerebral cortex is involved in sensory, motor, and integrative functions related to perception, voluntary musculoskeletal movements, and the broad range of activities associated with consciousness, language, emotions, and memory. The cerebrum functions in association with the lower centers of the nervous system. The lower areas of the brain such as the medulla, pons, mesencephalon, cerebellum, basal ganglia, substantia nigra, hypothalamus, and thalamus control unconscious activities including arterial pressure and respiration, equilibrium, and feeding reflexes, such as salivation.

The central nervous system (CNS) is composed of more than 100 billion neurons at the spinal cord level, the lower brain level, and the higher brain or cortical level. Neurons transmit electric or chemical signals between cells. The spinal cord, a thin, tubular extension of the central nervous system within the bony spinal canal, contains ascending sensory and descending motor pathways, and is covered by membranes continuous with those of the brainstem and cerebral hemispheres. The

spinal cord contains almost the entire motor output and sensory input systems of the trunk and limbs, and neuronal circuits in the cord also control rhythmic movements, such as walking, and a variety of reflexes. The lower areas of the brain such as the medulla, pons, mesencephalon, cerebellum, basal ganglia, substantia nigra, hypothalamus, and thalamus control unconscious activities including arterial pressure and respiration, equilibrium, and feeding reflexes, such as salivation. Emotions, such as anger, excitement, sexual response, and reaction to pain or pleasure, originate in the lower brain. The cerebral cortex or higher brain is the largest structure, consisting of a right and a left hemisphere interconnected by the corpus callosum. The cerebral cortex is involved in sensory, motor, and integrative functions related to perception, voluntary musculoskeletal movements, and the broad range of activities associated with consciousness, language, emotions, and memory. The cerebrum functions in association with the lower centers of the nervous system.

Nervous system organization and development

A nerve cell (neuron) contains four regions, the cell body, axon, dendrites, and axon terminal. The cell body contains the nucleus and other organelles. The dendrites are processes which extend outward from the cell body and receive signals from sense organs or from the axons of other neurons. These signals are converted to electrical impulses and transmitted to the cell body. The axon, whose size can range from one millimeter to more than one meter, is a single process that conducts the nerve impulse away from the cell body. Cytoskeletal fibers, including microtubules and neurofilaments, run the length of the axon and function in transporting proteins, membrane vesicles, and other macromolecules from the cell body along the axon to the axon terminal. Some axons are surrounded by a myelin sheath made up of membranes from either an oligodendrocyte cell (CNS) or a Schwann cell (PNS). Myelinated axons conduct electrical impulses faster than unmyelinated ones of the same diameter. The axon terminal is at the tip of the axon away from the cell body. (See Lodish, H. et al. (1986) Molecular Cell Biology Scientific American Books New York NY, pp. 715-719.)

CNS-associated proteins have roles in neuronal signaling, cell adhesion, nerve regeneration, axon guidance, neurogenesis, and other functions. Certain CNS-associated proteins form an integral part of a membrane or are attached to a membrane. For example, neural membrane protein 35 (NMP35) is closely associated with neuronal membranes and is known to be highly expressed in the rat adult nervous system (Schweitzer, B. et al. (1998) *Mol. Cell. Neurosci.* 11:260-273). Synaptophysin (SY) is a major integral membrane protein of small synaptic vesicles. The chromosomal location of SY in human and mouse is on the X chromosome in subbands Xp11.22-p11.23. This region has been implicated in several inherited diseases including Wiskott-Aldrich syndrome, three forms of X-linked hypercalciuric nephrolithiasis, and the eye disorders retinitis

pigmentosa 2, congenital stationary night blindness, and Aland Island eye disease (Fisher, S.E. et al. (1997) *Genomics* 45:340-347). Peripherin, or retinal degeneration slow protein (rds), is an integral membrane glycoprotein that is present in the rims of photoreceptor outer segment disks. In mammals, rds is thought to stabilize the disk rim through heterophilic interactions with related nonglycosylated proteins. Rds is a mouse neurological mutation that is characterized by abnormal development of rod and cone photoreceptors followed by their slow degeneration (Kedzierski, W.J. et al. (1999) *Neurochem.* 72:430-438).

Each of over a trillion neurons in adult humans connects with over a thousand target cells (Tessier-Lavigne, M. et al. (1996) *Science* 274:1123-1133). These neuronal connections form during embryonic development. Each differentiating neuron sends out an axon tipped at the leading edge by a growth cone. Aided by molecular guidance cues, the growth cone migrates through the embryonic environment to its synaptic target. Progressive axon outgrowth occurs during neural development but not in the mature mammalian CNS. Following CNS injury, expression of growth-inhibiting molecules is enhanced while availability of their growth-promoting counterparts diminishes. Proteins governing developmental axon guidance contribute to the failure of injured central neurons to regenerate. These proteins include Semaphorin3A and the Semaphorin3A receptor proteins neuropilin-1 and plexin-A1 (Pasterkamp, R.J. and J. Verhaagen (2001) *Brain Res. Brain Res. Rev.* 35:36-54).

Semaphorins function during embryogenesis by providing local signals to specify territories inaccessible to growing axons (Puschel, A.W. et al. (1995) *Neuron* 14:941-948). They consist of at least 30 different members and are found in vertebrates, invertebrates, and even certain viruses. All semaphorins contain the sema domain which is approximately 500 amino acids in length. Neuropilin, a semaphorin receptor, has been shown to promote neurite outgrowth *in vitro*. The extracellular region of neuropilins consists of three different domains: CUB, discoidin, and MAM domains. The CUB and the MAM motifs of neuropilin have been suggested to have roles in protein-protein interactions and are thought to be involved in the binding of semaphorins through the sema and the C-terminal domains (reviewed in Raper, J.A. (2000) *Curr. Opin. Neurobiol.* 10:88-94).

The guidance of axons during development involves both positive and negative effects (i.e., chemoattraction and chemorepulsion). The Slit family of proteins have been implicated in promoting axon branching, elongation, and repulsion. Members of the Slit family have been identified in a variety of organisms, including insects, amphibians, birds, rodents and humans (Guthrie, S. (1999) *Current Biology* 9:R432-R435). Slit proteins are ligands for the repulsive guidance receptor, Roundabout (Robo); however, Slit proteins also cause elongation in some assays. A post-translationally processed form of Slit appears to be the active form of the protein (Guthrie, S. *supra*; and Brose, K. et al. (1999)

Cell 96:795-806).

Axon growth is also guided in part by contact-mediated mechanisms involving cell surface and extracellular matrix (ECM) molecules. Many ECM molecules, including fibronectin, vitronectin, members of the laminin, tenascin, collagen, and thrombospondin families, and a variety of proteoglycans, can act either as promoters or inhibitors of neurite outgrowth and extension (Tessier-Lavigne et al., *supra*). Receptors for ECM molecules include integrins, immunoglobulin superfamily members, and proteoglycans. ECM molecules and their receptors have also been implicated in the adhesion, maintenance, and differentiation of neurons (Reichardt, L.F. et al. (1991) *Ann. Rev. Neurosci.* 14:531-571). The proteoglycan testican is localized to the post-synaptic area of pyramidal cells of the hippocampus and may play roles in receptor activity, neuromodulation, synaptic plasticity, and neurotransmission (Bonnet, F. et al. (1996) *J. Biol. Chem.* 271:4373-4380).

Other proteins involved in morphogenetic processes in neural tissues include members of the striatin family such as zinedin and striatin, and members of the sialoadhesins such as myelin-associated glycoprotein (MAG), Schwann cell myelin protein (SMP) and sialoadhesin. Zinedin and striatin are calmodulin-binding, WD repeat proteins primarily expressed in the brain (Castets, F. et al. (2000) *J. Biol. Chem.* 275:19970-19977). These two proteins share four homologous stretches of amino acids that have been determined to be involved in protein-protein interactions such as caveolin-binding and calmodulin-binding. Both zinedin and striatin have been shown to bind calmodulin in a Ca^{2+} -dependent manner. That striatin is possibly involved in the formation of dendrites has been demonstrated in cultured embryonic motoneurons in which striatin synthesis was specifically blocked. These cells had a reduced number of poorly branched dendrites, whereas the growth of axons appeared normal (Bartoli, M. et al. (1999) *J. Neurobiol.* 40:234-243). The role of striatin in the control of locomotion has been demonstrated in rats (Bartoli, M. et al. *supra*). The sialoadhesins are a major subgroup of the I-type lectins which are themselves a subfamily of the lectins. I-type lectins consist mainly of transmembranous glycoproteins belonging to the immunoglobulin superfamily. The sialoadhesins, myelin-associated glycoprotein (MAG), Schwann cell myelin protein (SMP) and sialoadhesin, are expressed in the nervous system and are generally characterized as sialic acid-binding adhesion molecules. MAG is expressed by oligodendrocytes in the CNS in L (large) and S (small) forms that are developmentally regulated such that the L form is expressed predominantly during early stages of myelination and the S form is primarily expressed in adulthood (Tropak, M.B. et al. (1988) *Mol. Brain Res.* 4:143-155; Pedraza, L. et al. (1991) *J. Neurosci. Res.* 29:141-148). MAG is also expressed in the Schwann cells in the peripheral nervous system (PNS) and has been implicated in cell recognition mechanisms underlying either the promotion or inhibition of cell adhesion and neurite outgrowth

(Martini, R. (1994) *J. Neurocytol.* 21:1-28; Bartsch, U. (1996) *J. Neurocytol.* 25:303-313). SMP is expressed by oligodendrocytes and in Schwann cells, has similar sialic acid-binding properties to MAG and shares 43.5% sequence identity with MAG (Dulac, C. et al. (1992) *Neuron* 8:323-334; Collins, B. E. et al. (1997) *J. Biol. Chem.* 272:16889-16895). Sialoadhesin is a membrane glycoprotein originally described as a cell surface receptor expressed by murine macrophages (Crocker, P.R. and Gordon, S. (1986) *J. Exp. Med.* 164:1862-1875; Crocker, P.R. and Gordon, S. (1989) *J. Exp. Med.* 169:1333-1346). Expression of sialoadhesin has since been demonstrated in rat macrophages which have been induced by glucocorticoids and can be further enhanced by the addition of interferon β or γ , interleukin 4 or lipopolysaccharides (Van den Berg T.K. et al. (1996) *J. Immunol.* 157:3130-3138). Expression patterns and binding specificities of sialoadhesin suggest a possible role in regulation of myeloid cell development (Crocker, P.R. et al. (1990) *Blood* 76:1131-1138; Crocker P.R. et al. (1995) *J. Clin. Invest.* 95:635-643).

Neurotrophins regulate development, maintenance, and function of vertebrate nervous systems. Neurotrophins activate two different classes of receptors, the Trk family of receptor tyrosine kinases and p75NTR, a member of the TNF receptor superfamily. Through these receptors, neurotrophins activate many signaling pathways, including those mediated by ras and members of the cdc-42/ras/rho G protein families, and by the MAP kinase, PI-3 kinase, and Jun kinase cascades. During development, limiting amounts of neurotrophins function as survival factors to ensure a match between the number of surviving neurons and the requirement for appropriate target innervation. They also regulate cell fate decisions, axon growth, dendrite pruning, the patterning of innervation, and the expression of proteins crucial for normal neuronal function, such as neurotransmitters and ion channels. These proteins also regulate many aspects of neural function. In the mature nervous system, they control synaptic function and synaptic plasticity, while continuing to modulate neuronal survival (Huang, E.J. and L.F. Reichardt (2001) *Ann. Rev. Neurosci.* 24:677-736). Neuritin is a protein induced by neural activity and by neurotrophins which promote neuritogenesis.

The neurexophilins are neuropeptide-like proteins which are proteolytically processed after synthesis. They are ligands for the neuron-specific cell surface proteins, the α -neurexins. Neurexophilins and neurexins may participate in a neuron signaling pathway (Missler, M. and T.C. Sudhof (1998) *J. Neurosci.* 18:3630-3638; Missler, M. et al. (1998) *J. Biol. Chem.* 273:34716-34723). Ninjurin is a neuron cell surface protein which plays a role in cell adhesion and in nerve regeneration following injury. Ninjurin is up-regulated after nerve injury in dorsal root ganglion neurons and in Schwann cells (Araki, T. and J. Milbrandt (1996) *Neuron* 17:353-361). Ninjurin2 is expressed in mature sensory and enteric neurons and promotes neurite outgrowth. Ninjurin2 is upregulated in

Schwann cells surrounding the distal segment of injured nerve with a time course similar to that of *ninjurin1*, *neural CAM*, and *L1* (Araki, T. and J. Milbrandt (2000) *J. Neurosci.* 20:187-195).

Neurexin IV is essential for axonal insulation in the PNS in embryos and larvae. Axonal insulation is of key importance for the proper propagation of action potentials. *Caspr*, a vertebrate
 5 homolog of Neurexin IV -- also named paranodin -- is found in septate-like junctional structures localized to the paranodal region of the nodes of Ranvier, between axons and Schwann cells. *Caspr*/paranodin is implicated in blood-brain barrier formation, and linkage of neuronal membrane components with the axonal cytoskeletal network (Bellen, H.J. et al. (1998) *Trends Neurosci.* 21:444-449).

10 Mammalian Numb is a phosphotyrosine-binding (PTB) domain-containing protein which may be involved in cortical neurogenesis and cell fate decisions in the mammalian nervous system. Numb's binding partner, the LNX protein, contains four PDZ domains and a ring finger domain and may participate in a signaling pathway involving Numb. PDZ domains have been found in proteins
 15 at surfaces of cell membranes (Ponting, C.P. (1997) *Bioessays* 19:469-479). LNX contains a tyrosine phosphorylation site which may be important for the binding of other PTB-containing proteins such as SHC, an adaptor protein which associates with tyrosine-phosphorylated growth factor receptors and downstream effectors (Dho, S.E. et al. (1998) *J. Biol. Chem.* 273:9179-9187).

Nogo has been identified as a component of the central nervous system myelin that prevents
 20 axonal regeneration in adult vertebrates. Cleavage of the Nogo-66 receptor and other glycoposphatidylinositol-linked proteins from axonal surfaces renders neurons insensitive to Nogo-66, facilitating potential recovery from CNS damage (Fournier, A.E. et al. (2001) *Nature* 409:341-346).

Homeobox transcription factors direct nerve-cell associated tissue patterning and differentiation. The presence and function of these proteins appears to be ubiquitous in nematodes,
 25 arthropods, and vertebrates. One example of these proteins is DRG11, a homeobox transcription factor expressed in mammalian sensory neurons, and which appears to be involved in neural crest development (Saito, T. et al. (1995) *Mol. Cell Neurosci.* 6:280-292). Cutaneous sensory neurons that detect noxious stimuli project to the dorsal horn of the spinal cord, while those innervating muscle stretch receptors project to the ventral horn. DRG11 is required for the formation of spatio-temporally
 30 appropriate projections from nociceptive sensory neurons to their central targets in the dorsal horn of the spinal cord (Chen, Z.F. et al. (2001) *Neuron* 31:59-73).

Synapses

Contact between one neuron and another occurs at a specialized site called the synapse.

Many nervous system functions are regulated by diverse synaptic proteins such as synaptophysin, the synapsins, growth associated protein 43 (GAP-43), SV-2, and p65, which are distributed in subcellular compartments of the synapse. Synaptic terminals also contain many other proteins involved in calcium transport, neurotransmission, signaling, growth, and plasticity. At this site, the axon terminal from one neuron (the presynaptic cell) sends a signal to another neuron (the postsynaptic cell). Synapses may be connected either electrically or chemically. An electrical synapse consists of gap junctions connecting the two neurons, allowing electrical impulses to pass directly from the presynaptic to the postsynaptic cell. In a chemical synapse, the axon terminal of the presynaptic cell contains membrane vesicles containing a particular neurotransmitter molecule. A change in electrical potential at the nerve terminal results in the influx of calcium ions through voltage-gated channels which triggers the release of the neurotransmitter from the synaptic vesicle by exocytosis. The neurotransmitter rapidly diffuses across the synaptic cleft separating the presynaptic nerve cell from the postsynaptic cell. The neurotransmitter then binds receptors and opens transmitter-gated ion channels located in the plasma membrane of the postsynaptic cell, provoking a change in the cell's electrical potential. This change in membrane potential of the postsynaptic cell may serve either to excite or inhibit further transmission of the nerve impulse.

Presynaptic calcium channel activity is modulated by cysteine-string proteins (CSPs). CSPs are secretory vesicle proteins that function in neurotransmission as well as in exocytosis in other cell-types. CSPs belong to the DnaJ/hsp40 (heat shock protein) chaperone family. The effect of CSPs on calcium levels is likely to be downstream of calcium release and is likely to involve exocytosis, possibly in connection with G-proteins (Braun, J.E. et al. (1995) *Neuropharmacology* 34:1361-9136; Magga, J.M. et al. (2000) *Neuron* 28:195-204; Dawson-Scully, K. et al. (2000) *J. Neurosci.* 20:6039-6047; and Chamberlain, L.H. et al. (2001) *J. Cell Sci.* 114:445-455). Neuregulins (NRGs) mediate between the electrical neural activity and molecular components by regulating the expression of ion channel receptors or transmitter release in synapses. NRGs may also be signaling factors involved in tuning locomotion or other higher functions by coordinating excitatory and inhibitory neurons (Ozaki, M. (2001) *Neuroscientist* 7:146-154).

N- and P/Q-type Ca^{2+} channels are localized in high density in presynaptic nerve terminals and are crucial elements in neuronal excitation-secretion coupling. In addition to mediating Ca^{2+} entry to initiate transmitter release, they are thought to interact directly with proteins of the synaptic vesicle docking/fusion machinery. N-type and P/Q-type Ca^{2+} channels are colocalized with syntaxin in high-density clusters in nerve terminals. The synaptic protein interaction (synprint) sites in the intracellular loop II-III (LII-III) of both alpha 1B and alpha 1A subunits of N-type and P/Q-type Ca^{2+}

channels bind to syntaxin, SNAP-25, and synaptotagmin. Presynaptic Ca^{2+} channels not only provide the Ca^{2+} signal required by the exocytotic machinery, but also contain structural elements that are integral to vesicle docking, priming, and fusion processes (Catterall, W.A. (1999) Ann. NY Acad. Sci. 868:144-159). Synaptotagmins are a large family of proteins involved in both regulated and

5 constitutive vesicular trafficking. They include a neuronal type (synaptotagmin I-V, X, and XI) and a ubiquitous type (synaptotagmin VI-IX). Ca^{2+} -dependent synaptotagmin activation is involved in neurite outgrowth (Mikoshiba, K. et al. (1999) Chem. Phys. Lipids 98:59-67).

Proteins associated with the membranes of synaptic vesicles include vamp (synaptobrevin), rab3A, synaptophysin, synaptotagmin (p65) and SV2. These membrane proteins function in regulated

10 exocytosis by regulating neurotransmitter uptake, vesicle targeting, and fusion with the presynaptic plasma membrane (Elferink, L.A. and R.H. Scheller (1993) J. Cell Sci. Suppl.17:75-79).

Physophilin, also known as the Ac39 subunit of the V-ATPase, is an oligomeric protein that binds the synaptic vesicle protein synaptophysin, constituting a complex that may form the exocytotic fusion pore. Ac39 is present in a synaptosomal complex which, in addition to synaptophysin, includes

15 the bulk of synaptobrevin II, and subunits c and Ac115 of the V0 sector of the V-ATPase. *In situ* hybridization in rat brain reveals a largely neuronal distribution of Ac39/physophilin mRNA which correlates spatio-temporally with those of subunit c and synaptophysin. Immunohistochemical analysis shows that Ac39/physophilin is mostly concentrated in the neuropil with a pattern identical to subunit A and very similar to synaptophysin. Double-labeling immunofluorescence shows a complete

20 colocalization of Ac39/physophilin with subunit A and a partial colocalization with synaptophysin in the neuropil (Carrion-Vazquez M. et al. (1998) Eur. J. Neurosci.10:1153-1166).

The plasma membrane dopamine transporter (DAT) is essential for the reuptake of released dopamine from the synapse. Uptake of dopamine is temperature- and time-dependent, and is inhibited by a variety of compounds, such as cocaine. DAT-knockout mice have been shown to exhibit

25 extreme hyperactivity and resistance to both cocaine and amphetamine, consistent with the primary action of cocaine on DAT (Giros, B. et al. (1996) Nature 379:606-612). The perturbation of the tightly regulated DAT also predisposes neurons to damage by a variety of insults. Most notable is the selective degeneration of DAT-expressing dopamine nerve terminals in the striatum thought to underlie Parkinson's disease. DAT expression can predict the selective vulnerability of neuronal

30 populations, which suggests that therapeutic strategies aimed at altering DAT function could have significant benefits in a variety of disorders (Gary, W.M. et al. (1999) Trends Pharmacol. Sci. 20:424-429).

43 KD postsynaptic protein or acetylcholine receptor-associated 43 KD protein (RAPSYN) is

thought to play a role in anchoring or stabilizing the nicotinic acetylcholine receptor at synaptic sites. RAPSYN is involved in membrane association and may link the nicotinic acetylcholine receptor to the underlying postsynaptic cytoskeleton (Buckel, A. et al. (1996) *Genomics* 35:613-616). Neuritin is a protein whose gene is known to be induced by neural activity and by neurotrophins which promote neuritogenesis. Neuraxin is a structural protein of the rat central nervous system that is believed to be immunologically related to microtubule-associated protein 5 (MAP5). Neuraxin is a novel type of neuron-specific protein which is characterized by an unusual amino acid composition, 12 central heptadecarepeats and putative protein and membrane interaction sites. The gene encoding neuraxin is unique in the haploid rat genome and is conserved in higher vertebrates. Neuraxin is implicated in neuronal membrane-microtubule interactions and is expressed throughout the rodent CNS (Rienitz, A. et al. (1989) *EMBO J.* 8:2879-2888).

Synaptic nuclear envelope-1 (Syne-1) protein is selectively associated with synaptic nuclei and may be involved in the formation or maintenance of nuclear aggregates at the neuromuscular junction. Syne-1 contains multiple spectrin repeats similar to those found in dystrophin and utrophin, as well as a domain homologous to the carboxyl-terminal of Klarsicht, a protein associated with nuclei and required for a subset of nuclear migrations in *Drosophila* (Apel, B. D. et al. (2000) *J. Biol. Chem.* 275:31986-31995.).

C1q-Related Factor (CRF) is found to be expressed at highest levels in the brain, particularly in the brainstem. In situ hybridization to mouse brain sections demonstrated that CRF transcripts are most abundant in areas of the nervous system involved in motor function, such as the Purkinje cells of the cerebellum, the accessory olivary nucleus, the pons and the red nucleus. CRF is predicted to encode a polypeptide with a hydrophobic signal sequence, a collagenous region, and a globular domain at the carboxy terminus that shares homology to the C1q signature domain, a subunit of the C1 enzyme complex that activates the serum complement system (Berube, N. G. et al. (1999) *Brain Res. Mol. Brain Res.* 63:233-240).

Neurotransmitters and neurotransmitter transport proteins

Contact from one neuron to another occurs at a specialized site called the synapse. At this site, the axon terminal from one neuron (the presynaptic cell) sends a signal to another neuron (the postsynaptic cell). Synapses may be connected either electrically or chemically. An electrical synapse consists of gap junctions connecting the two neurons, allowing electrical impulses to pass directly from the presynaptic to the postsynaptic cell. In a chemical synapse, the axon terminal of the presynaptic cell contains membrane vesicles containing a particular neurotransmitter molecule. A change in electrical potential at the nerve terminal results in the influx of calcium ions through voltage-

gated channels which triggers the release of the neurotransmitter from the synaptic vesicle by exocytosis. The neurotransmitter rapidly diffuses across the synaptic cleft separating the presynaptic nerve cell from the postsynaptic cell. The neurotransmitter then binds receptors and opens transmitter-gated ion channels located in the plasma membrane of the postsynaptic cell, provoking a change in the cell's electrical potential. This change in membrane potential of the postsynaptic cell may serve either to excite or inhibit further transmission of the nerve impulse. Presynaptic calcium channel activity is modulated by cysteine-string proteins (CSPs). CSPs are secretory vesicle proteins that function in neurotransmission as well as in exocytosis in other cell-types. CSPs belong to the DnaJ/hsp40 (heat shock protein) chaperone family. The effect of CSPs on calcium levels is likely to be downstream of calcium release and is likely to involve exocytosis, possibly in connection with G-proteins (Braun, J.E. et al. (1995) *Neuropharmacology* 34:1361-9136; Magga, J.M. et al. (2000) *Neuron* 28:195-204; Dawson-Scully, K. et al. (2000) *J. Neurosci.* 20:6039-6047; and Chamberlain, L.H. et al. (2001) *J. Cell Sci.* 114:445-455).

Neurotransmitters comprise a diverse group of some 30 small molecules which include acetylcholine, monoamines such as serotonin, dopamine, and histamine, and amino acids such as gamma-aminobutyric acid (GABA), glutamate, and aspartate, and neuropeptides such as endorphins and enkephalins (McCance, K.L. and S.E. Huether (1994) PATHOPHYSIOLOGY, The Biologic Basis for Disease in Adults and Children, 2nd edition, Mosby, St. Louis, MO, pp. 403-404). Many of these molecules have more than one function and the effects may be excitatory, e.g. to depolarize the postsynaptic cell plasma membrane and stimulate nerve impulse transmission, or inhibitory, e.g. to hyperpolarize the plasma membrane and inhibit nerve impulse transmission.

Neurotransmitters and their receptors are targets of pharmacological agents aimed at controlling neurological function. For example, GABA is the major inhibitory neurotransmitter in the CNS, and GABA receptors are the principal target of sedatives such as benzodiazepines and barbiturates which act by enhancing GABA-mediated effects (Katzung, B.G. (1995) Basic and Clinical Pharmacology, 6th edition, Appleton & Lange, Norwalk, CT, pp. 338-339).

Two major classes of neurotransmitter transporters are essential to the function of the nervous system. The first class is uptake carriers in the plasma membrane of neurons and glial cells, which pump neurotransmitters from the extracellular space into the cell. This process relies on the Na^+ gradient across the plasma membrane, particularly the co-transport of Na^+ . Two families of proteins have been identified. One family includes the transporters for GABA, monoamines such as noradrenaline, dopamine, and serotonin, and amino acids such as glycine and proline. Common structural components include twelve putative transmembrane α -helical domains, cytoplasmic N- and

C- termini, and a large glycosylated extracellular loop separating transmembrane domains three and four. This family of homologous proteins derives their energy from the co-transport of Na^+ and Cl^- ions with the neurotransmitter into the cell (Na^+/Cl^- neurotransmitter transporters). The second family includes transporters for excitatory amino acids such as glutamate. Common structural components
5 include 6-10 putative transmembrane domains, cytoplasmic N- and C- termini, and glycosylations in the extracellular loops. The excitatory amino acid transporters are not dependent on Cl^- , and may require intracellular K^+ ions (Na^+/K^+ - neurotransmitter transporters) (Liu, Y. et al. (1999) Trends Cell Biol. 9:356-363).

The second class of neurotransmitter transporters is present in the vesicle membrane, and
10 concentrates neurotransmitters from the cytoplasm into the vesicle, before exocytosis of the vesicular contents during synaptic transmission. Vesicular transport uses the electrochemical gradient across the vesicular membrane generated by a H^+ -ATPase. Two families of proteins are involved in the transport of neurotransmitters into vesicles. One family uses primarily proton exchange to drive transport into secretory vesicles and includes the transporters for monoamines and acetylcholine. For
15 example, the monoamine transporters exchange two luminal protons for each molecule of cytoplasmic transmitter. The second family includes the GABA transporter, which relies on the positive charge inside synaptic vesicles. The two classes of vesicular transporters show no sequence similarity to each other and have structures distinct from those of the plasma membrane carriers (Schloss, P. et al. (1994) Curr. Opin. Cell Biol. 6:595-599; Liu et al., *supra*).

20 GABA is the predominant inhibitory neurotransmitter and is widely distributed in the mammalian nervous system. GABA is cleared from the synaptic cleft by specific, high-affinity, Na^+ - and Cl^- - dependent transporters, which are thought to be localized to both pre- and postsynaptic neurons, as well as to surrounding glial cells. At least four GABA transporters (GAT1–GAT4) have been cloned (Liu, Q.-R. et al. (1993) J. Biol. Chem. 268:2106–2112). Studies of [^3H]-GABA uptake
25 into cultured cells and plasma-membrane vesicles isolated from various tissues revealed considerable differences in GABA transporter heterogeneity. GABA transporters exhibit differences in substrate affinity and specificity, distinct blocker pharmacologies, and different tissue localization. For example, the K_m values of GABA uptake of the expressed GAT1 to GAT4 are 6, 79, 18, and 0.8 mM, respectively. In addition to transporting GABA, GAT2 also transports betaine; GAT3 and GAT4 also
30 transport β -alanine and taurine. Pharmacological studies revealed that GABA transport by GAT1 and GAT4 is more sensitive to 2,4-diaminobutyric acid and guavicine than that by GAT2 and GAT3. *In situ* hybridization showed that GAT1 and GAT4 expression is brain specific. GAT2 and GAT3 mRNAs were detected in tissues such as liver and kidney (Schloss et al., *supra*; Borden, L.A. (1996)

Neurochem. Int. 29:335-356; Nelson, N. (1998) J. Neurochem. 71:1785-1803).

Human studies indicated that GABA transporter function is reduced in epileptic hippocampi. Decreased GABAergic neurotransmission has also been implicated in the pathophysiology of schizophrenia (Simpson, M.D. et al. (1992) Psychiatry Res. 42:273-282).

5 Diazepam binding inhibitor (DBI), also known as endozepine and acyl-Coenzyme (CoA)-binding protein, is an endogenous GABA receptor ligand which is thought to down-regulate the effects of GABA. DBI binds medium- and long-chain acyl-CoA esters with very high affinity and may function as an intracellular carrier of acyl-CoA esters (*125950 Diazepam Binding Inhibitor; DBI, Online Mendelian Inheritance in Man (OMIM); PROSITE PDOC00686 Acyl-CoA-binding protein
10 signature).

Glycine serves as one of the major inhibitory neurotransmitters in the mammalian nervous system by activating chloride-channel receptors, which are members of a ligand-gated ion-channel superfamily (Betz, H. (1990) Neuron 5:383-392). Glycine also facilitates excitatory transmission through an allosteric activation of the N-methyl-D-aspartate (NMDA) receptor (Johnson, J.W. and P.
15 Ascher (1987) Nature 325:529-531). Forms of glycine transporter include GLYT 1 and GLYT 2. Variants of GLYT1 (GLYT1 a/b) are generated by alternative splicing (Liu, Q.-R. et al. (1993) J. Biol. Chem. 268:22802-22808). GLYT1a is transcribed in both neural and non-neural tissues, whereas GLYT1b was detected only in neural tissues (Borowsky, B. et al. (1993) Neuron 10:851-863). High levels of GLYT1a/b-mRNA were found in hippocampus and cortex, implying its involvement in the
20 regulation of excitatory synaptic transmission. It is not clear whether GLYT1a is expressed in neurons, in glia or in both. In contrast, GLYT1b is found almost exclusively in fiber tracts, suggesting its localization in glial cells (Schloss et al., *supra*). GLYT2 is expressed mainly in brainstem and spinal cord (Schloss et al., *supra*).

The second identified glycine transporter (GLYT2) differs from GLYT1a/b by its extended
25 intracellular amino terminus. The predominant localization of its mRNA in brainstem and spinal cord and its insensitivity to N-methyl-aminoacetic acid suggests that GLYT2 terminates signal transduction at the strychnine-sensitive inhibitory glycine receptor. It has been proposed that, upon depolarization of cells harboring GLYT1b, the transporter runs backwards and releases glycine to act as a neuromodulatory amino acid at the NMDA receptor (Attwell, D. and M. Bouvier (1992) Curr. Biol.
30 2:541-543). Such a Ca^{2+} -independent, non-vesicular release of neurotransmitters by reverse transport was demonstrated for glutamate and serotonin. This evidence suggests that the transmitter transporters may be important for both the initiation and termination of neurotransmitter action (Schloss et al., *supra*).

The plasma membrane dopamine transporter (DAT) is essential for the reuptake of released dopamine from the synapse. Uptake of dopamine is temperature- and time-dependent, and is inhibited by a variety of compounds, such as cocaine. DAT- knockout mice have been shown to exhibit extreme hyperactivity and resistance to both cocaine and amphetamine, consistent with the primary
5 action of cocaine on DAT (Giros, B. et al. (1996) Nature 379:606-612). The perturbation of the tightly regulated DAT also predisposes neurons to damage by a variety of insults. Most notable is the selective degeneration of DAT-expressing dopamine nerve terminals in the striatum thought to underlie Parkinson's disease. DAT expression can predict the selective vulnerability of neuronal populations, which suggests that therapeutic strategies aimed at altering DAT function could have
10 significant benefits in a variety of disorders (Gary, W.M. et al. (1999) Trends Pharmacol. Sci. 20:424-429).

Creatine transporters are strongly related to transporters for GABA. The primary sequence identity between creatine transporter species homologs is very high (98-99%). Pharmacological characterization demonstrated high affinity creatine uptake (27-43 mM), which was blocked by
15 creatine analogs with high affinity. Creatine transporters are widely expressed in a variety of mammalian tissues, including brain, adrenal gland, intestine, colon, prostate, thymus, ovary, spleen, pancreas, placenta, umbilical cord, thyroid, tongue, pharynx, vertebral discs, jaw, and nasal epithelium. Genetic mapping in the mouse localizes the creatine transporter to a region on the X chromosome in linkage conservation with the human region Xq28, the location of the genes for several neuromuscular
20 diseases (Nash, S.R. et al. (1994) Receptors Channels 2:165-174).

The substrates of a number of cDNA clones encoding proteins of the Na⁺/Cl⁻-dependent transporter families are still not identified. These are orphan transporters. Identification of the substrates for orphan transporters has been difficult because *in situ* hybridization and immunohistochemistry indicate that the transporters are synthesized by phenotypically different
25 neuronal populations, for example glutaminergic, GABAergic, histaminergic, or serotonergic neurons. One of the transporters, NTT4, exhibits the highest homology to the creatine transporter. It differs structurally from other members of this family in having an unusually long loop between transmembranes seven and eight (Liu, Q.-R. et al. (1993) FEBS Lett. 315:114-118; Schloss et al., *supra*).

30 Glutamate is a major excitatory neurotransmitter in the mammalian central nervous system. Electrogenic (Na⁺/K⁺)-coupled glutamate transporters, located in the plasma membranes of nerve terminals and glial cells, mediate removal of glutamate released at excitatory synapses and maintain extracellular concentrations below neurotoxic levels. Glutamate transporters achieve this process by

co-transport with three sodium ions and one proton, followed by translocation of a potassium ion in the opposite direction (Zerangue, N. and M.P. Kavanaugh (1996) *Nature* 383:634-637).

Glutamate transporters belong to a large family of transport proteins. The membrane topology of the glutamate transporters reveals six membrane-spanning helices in the N-terminal part of the proteins (Slotboom, D.J. et al. (1999) *Microbiol. Mol. Biol. Rev.* 63:293-307). The C-terminal half of the glutamate transporters is well conserved and constitutes a major part of the translocation pathway and contains the binding sites for the substrate and co-transported ions (Zhang, Y. and B.I. Kanner (1999) *Proc. Natl. Acad. Sci. USA* 96:1710-1715).

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Impaired re-uptake of synaptic glutamate, and a reduced expression of glutamate transporters have been found in the motor cortex of patients with amyotrophic lateral sclerosis (ALS). Inhibition of the synthesis of each glutamate transporter subtype using chronic antisense oligonucleotide administration, *in vitro* and *in vivo*, selectively and specifically reduced the protein expression and function of glutamate transporters. The loss of glial glutamate transporters produced elevated extracellular glutamate levels, neurodegeneration characteristic of excitotoxicity, and a progressive paralysis. The loss of the neuronal glutamate transporter did not elevate extracellular glutamate in the striatum but produced mild neurotoxicity and resulted in epilepsy (Rothstein, J.D. et al. (1996) *Neuron* 16:675-686).

The vesicular monoamine transporters (VMAT) package cytoplasmic monoamine neurotransmitters into secretory vesicles for regulated exocytotic release. VMAT acts as an electrogenic exchanger of protons and monoamines, using a proton electrochemical gradient. VMAT transporters include VMAT1 and VMAT2. The VMAT proteins possess twelve transmembrane segments, with both extremities lying on the cytoplasmic side. VMAT proteins are associated with distinct vesicle populations in neurons and neuroendocrine cells (Henry, J.-P. et al. (1994) *J. Exp. Biol.* 196:251-262).

Vesicular transport is inhibited by the antihypertensive drug reserpine and the related but more centrally acting drug tetrabenazine. The mechanism of transport and the biochemistry of VMAT have been analyzed with these drugs, using mainly the chromaffin granules from bovine adrenal glands as a source of transporters (Peter, D. et al. (1994) *J. Biol. Chem.* 269:7231-7237).

Human studies indicated that reserpine can cause a syndrome resembling depression, indicating the importance of vesicular transport activity for the control of mood and behavior. The psychostimulant amphetamine also disrupts the storage of amines in secretory vesicles, further indicating that alterations in vesicular monoamine transport can affect behavior (Sulzer, D. and S. Rayport (1990) Neuron 5:797-808).

Human diseases caused by defects in neurotransmitter transporters include schizophrenia, Tourette's syndrome, Parkinson's disease, brain ischemia, amyotrophic lateral sclerosis, depression, and epilepsy. For example, decreased GABAergic neurotransmission has been implicated in the pathophysiology of CNS disorders such as epilepsy and schizophrenia. Impaired re-uptake of synaptic glutamate, and a reduced expression of the glutamate transporter have been found in the motor cortex of patients with amyotrophic lateral sclerosis (ALS). The loss of glial glutamate transporters produces elevated extracellular glutamate levels, neurodegeneration characteristic of excitotoxicity, and a progressive paralysis. The loss of neuronal glutamate transporters produces mild neurotoxicity and result in epilepsy (Rothstein, J.D. et al. (1996) Neuron 16:675-686).

Transporters for dopamine, norepinephrine, and serotonin have particular significance as targets for clinically relevant psychoactive agents including cocaine, antidepressants, and amphetamines. Cocaine and antidepressants are transporter antagonists that act with varying degrees of specificity to enhance synaptic concentrations of amines by limiting clearance. Amphetamines enhance transporter mediated efflux in concert with a depletion of vesicular amine stores (Barker, E.L. and R.D. Blakely (1995) Psychopharmacology 28:321-333; Sulzer, D. and S. Rayport (1990) Neuron 5:797-808; Wall, S.C. et al. (1995) Mol. Pharmacol. 47:544-550).

Each of over a trillion neurons in adult humans connects with over a thousand target cells (Tessier-Lavigne, M. et al. (1996) Science 274:1123-1133). These neuronal connections form during embryonic development. Each differentiating neuron sends out an axon tipped at the leading edge by a growth cone. Aided by molecular guidance cues, the growth cone migrates through the embryonic environment to its synaptic target. Semaphorins are growth cone guidance signals that may function during embryogenesis by providing local signals to specify territories inaccessible to growing axons (Puschel, A.W. et al. (1995) Neuron 14:941-948).

The guidance of axons during development involves both positive and negative effects (*i.e.*, chemoattraction and chemorepulsion). The Slit family of proteins have been implicated in promoting axon branching, elongation, and repulsion. Members of the Slit family have been identified in a variety of organisms, including insects, amphibians, birds, rodents and humans (Guthrie, S. (1999) Current Biology 9:R432-R435). Slit proteins appear to be ligands for the repulsive guidance receptor,

Roundabout (Robo); however, Slit proteins also cause elongation in some assays. A post-translationally processed form of Slit appears to be the active form of the protein (Guthrie, S. supra and Brose, K. et al. (1999) Cell 96:795-806).

Axon growth is also guided in part by contact-mediated mechanisms involving cell surface and
5 extracellular matrix (ECM) molecules. Many ECM molecules, including fibronectin, vitronectin, members of the laminin, tenascin, collagen, and thrombospondin families, and a variety of proteoglycans, can act either as promoters or inhibitors of neurite outgrowth and extension (Tessier-Lavigne et al., supra). Receptors for ECM molecules include integrins, immunoglobulin superfamily members, and proteoglycans. ECM molecules and their receptors have also been implicated in the
10 adhesion, maintenance, and differentiation of neurons (Reichardt, L.F. et al. (1991) Ann. Rev. Neurosci. 14:531-571). The proteoglycan testican is localized to the post-synaptic area of pyramidal cells of the hippocampus and may play roles in receptor activity, neuromodulation, synaptic plasticity, and neurotransmission (Bonnet, F. et al. (1996) J. Biol. Chem. 271:4373-4380).

Other nervous system-associated proteins have roles in neuron signaling, cell adhesion, nerve
15 regeneration, axon guidance, and neurogenesis. The neurexophilins are neuropeptide-like proteins which are proteolytically processed after synthesis. They are ligands for the neuron-specific cell surface proteins, the α -neurexins. Neurexophilins and neurexins may participate in a neuron signaling pathway (Missler, M. and T.C. Sudhof (1998) J. Neurosci. 18:3630-3638; Missler, M. et al. (1998) J. Biol. Chem. 273:34716-34723). Ninjurin is a neuron cell surface protein which plays a role in cell
20 adhesion and in nerve regeneration following injury. Ninjurin is up-regulated after nerve injury in dorsal root ganglion neurons and in Schwann cells (*602062 Ninjurin; NINJ1 OMIM; Araki, T. and Milbrandt, J. (1996) Neuron 17:353-361). Mammalian Numb is a phosphotyrosine-binding (PTB) domain-containing protein which may be involved in cortical neurogenesis and cell fate decisions in the mammalian nervous system. Numb's binding partner, the LNX protein, contains four PDZ domains
25 and a ring finger domain and may participate in a signaling pathway involving Numb. PDZ domains have been found in proteins which act as adaptors in the assembly of multifunctional protein complexes involved in signaling events at surfaces of cell membranes (Ponting, C.P. (1997) Bioessays 19:469-479). LNX contains a tyrosine phosphorylation site which may be important for the binding of other PTB-containing proteins such as SHC, an adaptor protein which associates with tyrosine-
30 phosphorylated growth factor receptors and downstream effectors (Dho, S.E. et al. (1998) J. Biol. Chem. 273:9179-9187).

Another family of molecules that appear to be important for neurotransmission are the choline-transporter-like CTL1 proteins. The prototypic CTL1 was identified in yeast as a suppressor

of a choline transport mutation; however, mammalian homologues have been identified. The proteins comprise approximately ten putative transmembrane domains in addition to transporter-like motifs but do not appear to be canonical choline transporters. Choline transport is important to neurotransmission because choline is a precursor of acetylcholine, required in abundance by cholinergic neurons

5 (O'Regan, S. et al. (2000) *Proc. Natl. Acad. Sci. U.S.A.* 97:1835-1840).

Transcriptional regulatory proteins are also essential for the development of the nervous system and elements of neurotransmission. A specific class of transcription factors, homeobox transcription factors, directs nerve cell-associated tissue patterning and differentiation. The presence and function of these proteins appears to be ubiquitous in nematodes, arthropods, and vertebrates.

10 One example of these proteins is DRG11, a homeobox transcription factor expressed in mammalian sensory neurons, and which appears to be involved in neural crest development (Saito, T. et al. (1995) *Mol. Cell Neurosci.* 6:280-292).

cDNA clones were selected by comparing libraries of normal mouse cerebellar cDNA and cerebellar cDNA from Purkinje cell degeneration (pcd) mice. An mRNA present in Purkinje neurons
15 encodes PCD5, a protein of 99 amino acids. PCD5's expression is restricted to the cerebellum and the eye. The gene encoding PCD5 was localized to mouse chromosome 8 (Nordquist, D.T. et al. (1988) *J. Neurosci.* 8(12):4780-4789).

Neuronal signals are transmitted across the neuromuscular junction (NMJ). Motor axons release the molecule agrin to induce the formation of the postsynaptic apparatus in muscle fibers.

20 Proteins such as dystroglycan, MuSK, and rapsyn participate in the transduction of agrin signals. Agrin also functions in the upregulation of gene transcription in myonuclei and the control of presynaptic differentiation (Ruegg, M.A. and J.L. Bixby (1998) *Trends Neurosci.* 21:22-27).

Neurological protein domains

CNS-associated proteins can be phosphoproteins. For example, ARPP-21 (cyclic
25 AMP-regulated phosphoprotein) is a cytosolic neuronal phosphoprotein that is highly enriched in the striatum and in other dopaminergic regions of the brain. The steady-state level of ARPP-21 mRNA is developmentally regulated. But, in the neonatal and mature animal, ARPP-21 mRNA is not altered following 6-hydroxydopamine lesions of the substantia nigra or by pharmacologic treatments that upregulate the D1- or D2-dopamine receptors (Ehrlich, M.E. et al. (1991) *Neurochem.* 57:1985-
30 1991).

CNS-associated signaling proteins may contain PDZ domains. PDZ domains have been found in proteins which act as adaptors in the assembly of multifunctional protein complexes involved in signaling events at surfaces of cell membranes. PDZ domains are generally found in membrane-

associated proteins including neuronal nitric oxide synthase (NOS) and several dystrophin-associated proteins (Ponting, C.P. et al. (1997) Bioessays 19:469-479). PSD-95/SAP90 is a membrane-associated guanylate kinase found in neuronal cells at the postsynaptic density (PSD) (Takeuchi, M. et al. (1997) J. Biol. Chem. 272:11943-11951). PSD-95/SAP90 contains three PDZ domains, one SH3
5 domain, and one guanylate kinase domain. The PDZ domains mediate interactions with NMDA receptors, Shaker-type potassium channels, and brain nitric oxide synthase. SAPAPs (SAP90/PSD-95-Associated Proteins) promote localization of PSD-95/SAP90 at the plasma membrane.

CNS-associated proteins may also contain epidermal growth factor (EGF) domains. The Notch proteins are transmembrane proteins which contain extracellular regions of repeated EGF
10 domains. Notch proteins, such as the *Drosophila melanogaster* neurogenic protein Notch, are generally involved in the inhibition of developmental processes. Other members of the Notch family are the *lin-12* and *glp-1* genes of *Caenorhabditis elegans*. Genetic studies indicate that the *lin-12* and *glp-1* proteins act as receptors in specific developmental cell interactions which may be involved in certain embryonic defects (Tax, F. E. et al. (1994) Nature 368:150-154). Pecanex, a maternal-effect
15 neurogenic locus of *D. melanogaster*, is believed to encode a large transmembrane protein. In the absence of maternal expression of the pecanex gene, an embryo develops severe hyperneuralization similar to that characteristic of Notch mutant embryos (LaBonne, S. G. et al. (1989) Dev. Biol. 136:1-116).

Other CNS-associated signaling proteins contain WW domains. The WW domain is a protein
20 motif with two highly conserved tryptophans. It is present in a number of signaling and regulatory proteins, including Huntingtin interacting protein. Several fibroblast growth factor (FGF) homologous factors (i.e., FHF polypeptides) have also been implicated in nervous system development based on mRNA expression patterns in mouse and human tissues. Members of the FHF family of polypeptides are structurally distinct from prototypic FGFs, consistent with the unusual role of these FGF-related
25 proteins (Smallwood, P.M. et al. (1996) Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857 and Hartung, H. et al. (1997) Mech. Dev. 64:31-39).

CNS-associated proteins may also contain leucine rich repeats (LRR) which are short motifs found in numerous proteins from a wide range of species. LRR motifs are of variable length, most commonly 20-29 amino acids, and multiple repeats are typically present in tandem. LRR motifs are
30 important for protein/protein interactions, and LRR proteins are involved in cell/cell interactions, morphogenesis, and development (Kobe, B. and Deisenhofer, J. (1995) Curr. Opin. Struct. Biol. 5:409-416). The human ISLR (immunoglobulin superfamily containing leucine-rich repeat) protein contains a C2-type immunoglobulin domain as well as LRR motifs. The ISLR gene is linked to the critical region

for Bardet-Biedl syndrome, a developmental disorder of which the most common feature is retinal dystrophy (Nagasawa, A. et al. (1999) *Genomics* 61:37-43). Brain leucine rich repeat protein, a member of the LRR family of proteins, possibly functions in nervous system development and maintenance (Taniguchi, H. et al. (1996) *Brain Res. Mol. Brain Res.* 36:45-52).

5 Disorders associated with neurological processes

Alzheimer's disease (AD) is a degenerative disorder of the CNS which causes progressive memory loss and cognitive decline during mid to late adult life. AD is characterized by a wide range of neuropathologic features including amyloid deposits and intra-neuronal neurofibrillary tangles. Although the pathogenic pathway leading to neurodegeneration and AD is not well understood, at least
10 three genetic loci that confer genetic susceptibility to the disease have been identified (Schellenberg, G.D. (1995) *Proc. Natl. Acad. Sci.* 92:8552-8559; Sherrington, R. et al. (1995) *Nature* 375:754-760).

Familial British dementia (FBD), is an autosomal dominant disease featuring amyloid plaques surrounded by astrocytes and microglia, neurofibrillary tangles, neuronal loss, and progressive dementia. The BRI gene on chromosome 13 encodes a 4 kD peptide, A-Bri. This membrane-
15 anchored protein is a primary constituent of amyloid deposits, and its presence in lesions from the CNS of FBD patients may be a contributive factor of this disease (El-Agnaf, O.M.A. et al. (2001) *Biochemistry* 40:3449-3457).

Astrocytomas, and the more malignant glioblastomas, are the most common primary tumors of the brain, accounting for over 65% of primary brain tumors. These tumors arise in glial cells of the
20 astrocyte lineage. Following infection by pathogens, astrocytes function as antigen-presenting cells and modulate the activity of lymphocytes and macrophages. Astrocytomas constitutively express many cytokines and interleukins that are normally produced only after infection by a pathogen (de Micco, C. (1989) *J. Neuroimmunol.* 25:93-108). In the course of identifying genes related to astrocyte differentiation, one cDNA was isolated from an astrocytoma cDNA library that encodes a protein
25 structurally related to the plant pathogenesis-related (PR) proteins (Murphy, E.V. et al. (1995) *Gene* 159:131-135). The glioma pathogenesis-related protein (GliPR) is highly expressed in glioblastoma, but not in fetal or adult brain, or in other nervous system tumors. PR proteins are a family of small (10-20 kDa), protease resistant proteins induced in plants by viral infections, such as tobacco mosaic virus. The synthesis of PR proteins is believed to be part of a primitive immunological response in
30 plants (van Loon, L.C. (1985) *Plant Mol. Biol.* 4:111-116). GliPR shares up to 50% homology with the PR-1 protein family over a region that comprises almost two thirds of the protein, including a conserved triad of amino acids, His-Glu-His, appropriately spaced to form a metal-binding domain (Murphy et al., *supra*).

Signaling initiated by the Trk family receptors plays a dynamic role in neurogenic tumors. The proto-oncogene Trks encode the high-affinity receptor tyrosine kinases for nerve growth factor (NGF) neurotrophins. A rearranged Trk oncogene is often observed in non-neuronal neoplasms such as colon and papillary thyroid cancers. The proto-oncogene Trks regulates growth, differentiation and apoptosis of tumors of neuronal origin, such as neuroblastoma and medulloblastoma (Nakagawara, A. (2001) Cancer Lett. 169:107-114).

Neuronal thread proteins (NTP) are a group of immunologically related molecules found in the brain and neuroectodermal tumor cell lines. NTP expression is increased in neuronal cells during proliferation, differentiation, brain development, in Alzheimer's disease (AD) brains, and in pathological states associated with regenerative nerve sprouting (de la Monte, S.M. et al. (1996) J. Neuropathol. Exp. Neurol. 55:1038-1050). Monoclonal antibodies generated to a recombinant NTP, AD7c-NTP, isolated from an end-stage AD brain library, showed high levels of NTP immunoreactivity in perikarya, neuropil fibers, and white matter fibers of AD brain tissue. *In vitro* studies also demonstrated NTP upregulation, phosphorylation, and translocation from the perikarya to cell processes and growth cones during growth factor-induced neuritic sprouting and neuronal differentiation. Additionally, increased NTP immunoreactivity was found in Down syndrome brains beginning in the second decade, prior to establishment of widespread AD neurodegeneration, and at an age when a low-level or an absence of NTP expression was observed in control brains. These findings indicated that abnormal expression and accumulation of NTP in brain may be an early marker of AD neurodegeneration in Down syndrome (de la Monte, S.M. et al. (1996) J. Neurol. Sci. 135:118-125). Furthermore, the increased expression and accumulation of NTP in AD brain tissue was paralleled by corresponding elevations of NTP in cerebrospinal fluid (CSF), and elevated levels of NTP were detectable in the CSF early in the course of the disease.

Ubiquilin is a presenilin-interacting protein. Ubiquilin contains numerous ubiquitin-like domains thought to be involved in targeting proteins for degradation. However, ubiquilin promotes increased presenilin protein accumulation. Ubiquilin, as a modulator of presenilin levels may have implications involving various cellular functions. Presenilins are linked to a variety of biological processes, including calcium regulation, Notch signaling, apoptosis, regulation of the cell cycle, including the unfolded-protein response and β -amyloid precursor protein-associated gamma secretase activity. Expression of ubiquilin is highest in human brain neurons and is associated with neurofibrillary tangles and Lewy bodies of Alzheimer's disease and Parkinson's disease brains, respectively (Mah, A.L., et al. (2000) J. Cell Biol. 151:847-862).

Fe65-like protein (Fe65L2), a new member of the Fe65 protein family, is one of the ligands

that interacts with the cytoplasmic domain of Alzheimer beta-amyloid precursor protein (APP). Transgenic mice expressing APP simulate some of the prominent behavioral and pathological features of Alzheimer's disease, including age-related impairment in learning and memory, neuronal loss, gliosis, neuritic changes, amyloid deposition, and abnormal tau phosphorylation (Duilio, A. et al. (1998)

5 Biochem. J. 330:513-519).

Amyotrophic lateral sclerosis (ALS) is characterized by motor neuron death, altered peroxidase activity of mutant SOD1, changes in intracellular copper homeostasis, protein aggregation, and changes in the function of glutamate transporters leading to excitotoxicity. Neurofilaments and peripherin appear to play some part in motor neuron degeneration. ALS is occasionally associated
10 with mutations of the neurofilament heavy chain gene (Al-Chalabi, A. and P.N. Leigh (2000) Curr. Opin. Neurol. 13:397-405). Cytoskeletal abnormalities such as abnormal inclusions containing neurofilaments (NFs) and/or peripherin, reduced mRNA levels for the NF light (NF-L) protein and mutations in the NF heavy (NF-H) gene have been observed in ALS. Intermediate filament inclusions containing peripherin may play a contributory role in ALS (Julien, J.P. and J.M. Beaulieu (2000) J.
15 Neurol. Sci.180:7-14).

Miller-Dieker syndrome (MDS) or isolated lissencephaly syndrome (ILS) are characterized by a smooth cerebral surface, a thickened cortex with four abnormal layers, and misplaced neurons. Both conditions may result from deletion or mutation in the LIS1 gene. The lissencephaly gene product Lis1 is a component of evolutionarily conserved intracellular multiprotein complexes essential
20 for neuronal migration, and which may be components of the machinery for cell proliferation and intracellular transport (Leventer, R.J. et al. (2001) Trends Neurosci. 24:489-492). NudC, a nuclear movement protein, interacts with Lis1 (Morris, S.M. et al. (1998) Curr. Biol. 8:603-606).

CNS-associated proteins can also be phosphoproteins. For example, ARPP-21 (cyclic AMP-regulated phosphoprotein) is a cytosolic neuronal phosphoprotein that is highly enriched in the
25 striatum and in other dopaminergic regions of the brain. The steady-state level of ARPP-21 mRNA is developmentally regulated. But, in the neonatal and mature animal, ARPP-21 mRNA is not altered following 6-hydroxydopamine lesions of the substantia nigra or by pharmacologic treatments that upregulate the D1- or D2-dopamine receptors. (Ehrlich, M. E. et al. (1991) Neurochem. 57:1985-1991.)

30 Retinitis pigmentosa comprises a group of slowly progressive, inherited disorders of the retina that cause loss of night vision and peripheral visual field in adolescence. A recessive nonsense mutation in the *Drosophila* opsin gene causes photoreceptor degeneration. In some families, genes encoding rhodopsin and peripherin/RDS map very close to the disease loci. Rhodopsin and

peripherin/RDS mutations have been found in approximately 30% of all autosomal dominant cases (Shastry, B.S. (1994) *Am. J. Med. Genet.* 52:467-474).

Astrocytomas, and the more malignant glioblastomas are primary tumors of the brain. The glioma pathogenesis-related protein (GliPR) is highly expressed in glioblastoma, but not in fetal or adult
5 brain, or in other nervous system tumors (Murphy, E.V. et al. (1995) *Gene* 159:131-135). Signaling initiated by the Trk family receptors plays a dynamic role in neurogenic tumors. The proto-oncogene Trks encode the high-affinity receptor tyrosine kinases for nerve growth factor (NGF) neurotrophins. A rearranged Trk oncogene is often observed in non-neuronal neoplasms such as colon and papillary thyroid cancers. The proto-oncogene Trks regulates growth, differentiation and apoptosis of tumors of
10 neuronal origin, such as neuroblastoma and medulloblastoma (Nakagawara, A. (2001) *Cancer Lett.* 169:107-114).

Synaptic proteins are involved in Alzheimer's disease (AD) and other disorders including ischemia, a variety of disorders where synapse-associated proteins are abnormally accumulated in the nerve terminals or synaptic proteins are altered after denervation, and neoplastic disorders (Masliah,
15 E. and R. Terry (1993) *Brain Pathol.* 3:77-85). Synaptophysin (SY), a major integral membrane protein of small synaptic vesicles, is on the X chromosome in subbands Xp11.22-p11.23, a region implicated in several inherited diseases including Wiskott-Aldrich syndrome, three forms of X-linked hypercalciuric nephrolithiasis, and the eye disorders retinitis pigmentosa 2, congenital stationary night blindness, and Aland Island eye disease (Fisher, S.E. et al. (1997) *Genomics* 45:340-347).

20 Mutations in the BRI2 isoform of the BRI gene family are associated with dementia in humans (Vidal, R. et al. (2001) *Gene* 266:95-102).

Changes in the molecular and cellular components of neuronal signaling systems correlate with the effects on mood and cognition observed after long-term treatment with antidepressant drugs. Two serine/threonine kinases, Ca^{2+} /calmodulin-dependent protein kinase II and cyclic AMP-dependent
25 protein kinase, are activated in the brain following antidepressant treatment. Associated changes in the phosphorylation of selected protein substrates in subcellular compartments including presynaptic terminals and microtubules may contribute to the modulation of synaptic transmission observed with antidepressants (Popoli, M. et al. (2001) *Pharmacol. Ther.* 89:149-170). Reserpine can cause a syndrome resembling depression, indicating the importance of vesicular transport activity for the
30 control of mood and behavior. The psychostimulant amphetamine also disrupts the storage of amines in secretory vesicles, further indicating that alterations in vesicular monoamine transport can affect behavior (Sulzer, D. and S. Rayport (1990) *Neuron* 5:797-808).

Decreased GABAergic neurotransmission has been implicated in the pathophysiology of CNS

disorders such as epilepsy and schizophrenia. Impaired re-uptake of synaptic glutamate and a reduced expression of the glutamate transporter have been found in the motor cortex of patients with amyotrophic lateral sclerosis (ALS). The loss of glial glutamate transporters produces elevated extracellular glutamate levels, neurodegeneration characteristic of excitotoxicity, and a progressive paralysis. The loss of neuronal glutamate transporters produces mild neurotoxicity and results in epilepsy (Rothstein, J.D. et al. (1996) *Neuron* 16:675-686). GABA transporter function is reduced in epileptic hippocampi. Transporters for dopamine, norepinephrine, and serotonin have particular significance as targets for clinically relevant psychoactive agents including cocaine, antidepressants, and amphetamines. Cocaine and antidepressants are transporter antagonists that act with varying degrees of specificity to enhance synaptic concentrations of amines by limiting clearance. Amphetamines enhance transporter mediated efflux in concert with a depletion of vesicular amine stores (Barker, E.L. and R.D. Blakely (1995) *Psychopharmacology* 28:321-333; Sulzer, D. and S. Rayport (1990) *Neuron* 5:797-808; Wall, S.C. et al. (1995) *Mol. Pharmacol.* 47:544-550).

The μ -opioid receptor (MOR) mediates the actions of analgesic agents including morphine, codeine, methadone, and fentanyl as well as heroin. MOR is functionally coupled to a G-protein-activated potassium channel (Mestek A. et al. (1995) *J. Neurosci.* 15:2396-2406). A variety of MOR subtypes exist. Alternative splicing has been observed with MOR-1 as with a number of G protein-coupled receptors including somatostatin 2, dopamine D2, prostaglandin EP3, and serotonin receptor subtypes 5-hydroxytryptamine4 and 5-hydroxytryptamine7 (Pan, Y.X. et al. (1999) *Mol. Pharm.* 56:396-403).

The central nervous system regulates the innate immune system by elaborating anti-inflammatory hormone cascades in response to bacterial products and immune mediators. The central nervous system also responds via acetylcholine-mediated efferent signals carried through the vagus nerve. Nicotinic cholinergic receptors expressed on macrophages detect these signals and respond with a dampened cytokine response (Tracey K.J. et al. (2001) *FASEB J.* 15:1575-1576).

Machado-Joseph disease (MJD) is an autosomal dominant, neurodegenerative disorder characterized by cerebellar ataxia, pyramidal and extra-pyramidal signs, peripheral nerve palsy, external ophthalmoplegia, facial and lingual fasciculation and bulging. The MJD josphin protein (amino acid residues 29-62) is a predominantly cytoplasmic protein associated with human neurons, but also detected in the nuclei of neurons and glial cells (Mruk, D.D. and Cheng, C.Y. (1999) *J. Biol. Chem.* 274:27056-27068).

Juvenile neuronal ceroid lipofuscinosis (JNCL), also known as Batten disease, is an autosomal

recessive lysosomal storage disease associated with mutations in CLN3. The predominant mutation in CLN3 is a 1.02 kb genomic deletion that accounts for nearly 85% of the disease alleles. Additional missense and nonsense mutations have been described. Some missense substitutions result in a protracted phenotype, with delays in the onset of classical clinical features, whereas others lead to classical JNCL. CLN3 is a hydrophobic protein containing 5 to 7 transmembrane domains. CLN3 is found to be highly associated with lysosome-associated membrane protein II in non-neuronal cells and with synaptophysin in neuronal cell lines (Haskell, R.E. et al. (2000) Hum. Mol. Genet. 9:735-744).

Dysferlin is the protein product of the gene mutated in patients with an autosomal recessive limb-girdle muscular dystrophy type 2B (LGMD2B) and a distal muscular dystrophy, Miyoshi myopathy. Dysferlin is homologous to a *Caenorhabditis elegans* spermatogenesis factor, FER-1. Otoferlin, another human FER-1-like protein (ferlin), is responsible for autosomal recessive nonsyndromic deafness (DFNB9). All the ferlins are characterized by sequences corresponding to multiple C2 domains that share the highest level of homology with the C2A domain of rat synaptotagmin III (Britton S. et al. (2000) Genomics 68:313-321).

15 Expression profiling

Microarrays are analytical tools used in bioanalysis. A microarray has a plurality of molecules spatially distributed over, and stably associated with, the surface of a solid support. Microarrays of polypeptides, polynucleotides, and/or antibodies have been developed and find use in a variety of applications, such as gene sequencing, monitoring gene expression, gene mapping, bacterial identification, drug discovery, and combinatorial chemistry.

One area in particular in which microarrays find use is in gene expression analysis. Array technology can provide a simple way to explore the expression of a single polymorphic gene or the expression profile of a large number of related or unrelated genes. When the expression of a single gene is examined, arrays are employed to detect the expression of a specific gene or its variants. When an expression profile is examined, arrays provide a platform for identifying genes that are tissue specific, are affected by a substance being tested in a toxicology assay, are part of a signaling cascade, carry out housekeeping functions, or are specifically related to a particular genetic predisposition, condition, disease, or disorder.

Lung Cancer

Lung cancer is the leading cause of cancer death for men and the second leading cause of cancer death for women in the U.S. The vast majority of lung cancer cases are attributed to smoking tobacco, and increased use of tobacco products in third world countries is projected to lead to an

epidemic of lung cancer in these countries. Exposure of the bronchial epithelium to tobacco smoke appears to result in changes in tissue morphology, which are thought to be precursors of cancer. Lung cancers are divided into four histopathologically distinct groups. Three groups (squamous cell carcinoma, adenocarcinoma, and large cell carcinoma) are classified as non-small cell lung cancers (NSCLCs). The fourth group of cancers is referred to as small cell lung cancer (SCLC). Collectively, NSCLCs account for ~70% of cases while SCLCs account for ~18% of cases. The molecular and cellular biology underlying the development and progression of lung cancer are incompletely understood.

Deletions on chromosome 3 are common in this disease and are thought to indicate the presence of a tumor suppressor gene in this region. Activating mutations in K-ras are commonly found in lung cancer and are the basis of one of the mouse models for the disease.

Ovarian Cancer

Ovarian cancer is the leading cause of death from a gynecologic cancer. The majority of ovarian cancers are derived from epithelial cells, and 70% of patients with epithelial ovarian cancers present with late-stage disease. As a result, the long-term survival rates for this disease is very low. Identification of early-stage markers for ovarian cancer would significantly increase the survival rate. The molecular events that lead to ovarian cancer are poorly understood. Some of the known aberrations include mutation of p53 and microsatellite instability. Since gene expression patterns are likely to vary when normal ovary is compared to ovarian tumors, examination of gene expression in these tissues to identify possible markers for ovarian cancer is particularly relevant to improving diagnosis, prognosis, and treatment of this disease.

Colon Cancer

Colorectal cancer is the second leading cause of cancer deaths in the United States. Colon cancer is associated with aging, since 90% of the total cases occur in individuals over the age of 55. A widely accepted hypothesis is that several contributing genetic mutations must accumulate over time in an individual who develops the disease. To understand the nature of genetic alterations in colorectal cancer, a number of studies have focused on the inherited syndromes. The first known inherited syndrome, Familial Adenomatous Polyposis (FAP), is caused by mutations in the Adenomatous Polyposis Coli gene (APC), resulting in truncated or inactive forms of the protein. This tumor suppressor gene has been mapped to chromosome 5q. The second known inherited syndrome is hereditary nonpolyposis colorectal cancer (HNPCC), which is caused by mutations in mismatch repair genes.

Although hereditary colon cancer syndromes occur in a small percentage of the population and most colorectal cancers are considered sporadic, knowledge from studies of the hereditary syndromes can be generally applied. For instance, somatic mutations in APC occur in at least 80% of indiscriminate colon tumors. APC mutations are thought to be the initiating event in the disease.

- 5 Other mutations occur subsequently. Approximately 50% of colorectal cancers contain activating mutations in ras, while 85% contain inactivating mutations in p53. Changes in these genes lead to gene expression changes in colon cancer. Less is understood about downstream targets of these mutations and the role they may play in cancer development and progression.

Tangier Disease

- 10 Tangier disease (TD) is a rare genetic disorder characterized by near absence of circulating high density lipoprotein (HDL) and the accumulation of cholesterol esters in many tissues, including tonsils, lymph nodes, liver, spleen, thymus, and intestine. Low levels of HDL represent a clear predictor of premature coronary artery disease and homozygous TD correlates with a four- to six-fold increase in cardiovascular disease compared to controls. The major cardio-protective activity of HDL
- 15 is ascribed to its role in reverse cholesterol transport, the flux of cholesterol from peripheral cells such as tissue macrophages, through plasma lipoproteins to the liver. The HDL protein, apolipoprotein A-I, plays a major role in this process, interacting with the cell surface to remove excess cholesterol and phospholipids. Recent studies have shown that this pathway is severely impaired in TD and the defect lies in a specific gene, the ABC1 transporter. This gene is a member of the family of ATP-binding
- 20 cassette transporters, which utilize ATP hydrolysis to transport a variety of substrates across membranes.

RNA Expression

- Atherosclerosis and the associated coronary artery disease and cerebral stroke represent the most common cause of death in industrialized nations. Although certain key risk factors have been
- 25 identified, a full molecular characterization that elucidates the causes and provide care for this complex disease has not been achieved. Molecular characterization of growth and regression of atherosclerotic vascular lesions requires identification of the genes that contribute to features of the lesion including growth, stability, dissolution, rupture and, most lethally, induction of occlusive vessel thrombus.

- 30 An early step in the development of atherosclerosis is formation of the "fatty streak". Lipoproteins, such as the cholesterol-rich low-density lipoprotein (LDL), accumulate in the extracellular space of the vascular intima, and undergo modification. Oxidation of LDL occurs most

avidly in the sub-endothelial space where circulating antioxidant defenses are less effective. The degree of LDL oxidation affects its interaction with target cells. "Minimally oxidized" LDL (MM-LDL) is able to bind to LDL receptor but not to the oxidized LDL (Ox-LDL) or "scavenger" receptors that have been identified, including scavenger receptor types A and B, CD36 ,

5 CD68/macrosialin and LOX-1 (Navab *et al.* (1994) *Arterioscler Thromb Vasc Biol* 16:831-842; Kodama *et al.* (1990) *Nature* 343:531-535; Acton *et al.* (1994) *J Biol Chem* 269:21003-21009; Endemann *et al.* (1993) *J Biol Chem* 268:11811-11816; Ramprasad *et al.* (1996) *Proc Natl Acad Sci* 92:14833-14838; Kataoka *et al.* (1999) *Circulation* 99:3110-3117). MM-LDL can increase the adherence and penetration of monocytes, stimulate the release of monocyte chemotactic protein 1

10 (MCP-1) by endothelial cells, and induce scavenger receptor A (SRA) and CD36 expression in macrophages (Cushing *et al.* (1990) *Proc Natl Acad Sci* 87:5134-5138; Yoshida *et al.* (1998) *Arterioscler Thromb Vasc Biol* 18:794-802; Steinberg (1997) *J Biol Chem* 272:20963-20966). SRA and the other scavenger receptors can bind Ox-LDL and enhance uptake of lipoprotein particles.

Mononuclear phagocytes enter the intima, differentiate into macrophages, and ingest modified

15 lipids including Ox-LDL. In most cell types, cholesterol content is tightly controlled by feedback regulation of LDL receptors and biosynthetic enzymes (Brown and Goldstein (1986) *Science* 232:34-47). In macrophages, however, the additional scavenger receptors lead to unregulated uptake of cholesterol (Brown and Goldstein (1983) *Annu Rev Biochem* 52:223-261) and accumulation of multiple intracellular lipid droplets producing a "foam cell" phenotype. Cholesterol-engorged and dead

20 macrophages contribute most of the mass of early "fatty streak" plaques and typical "advanced" lesions of diseased arteries. Numerous studies have described a variety of foam cell responses that contribute to growth and rupture of atherosclerotic vessel wall plaques. These responses include production of multiple growth factors and cytokines, which promote proliferation and adherence of neighboring cells; chemokines, which further attract circulating monocytes into the growing plaque;

25 proteins, which cause remodeling of the extracellular matrix; and tissue factor, which can trigger thrombosis (Ross (1993) *Nature* 362:801-809; Quin *et al.* (1987) *Proc Natl Acad Sci* 84:2995-2998). Thus, cholesterol-loaded macrophages which occur in abundance in most stages of the atherosclerotic plaque formation contribute to inception of the atherosclerotic process and to eventual plaque rupture and occlusive thrombus.

30 During Ox-LDL uptake, macrophages produce cytokines and growth factors that elicit further cellular events that modulate atherogenesis such as smooth muscle cell proliferation and production of extracellular matrix. Additionally, these macrophages may activate genes involved in inflammation

including inducible nitric oxide synthase. Thus, genes differentially expressed during foam cell formation may reasonably be expected to be markers of the atherosclerotic process.

Association of NTRAN polynucleotides with Parkinson's Disease

Several genes have been identified as showing linkage to autosomal dominant forms of
5 Parkinson's Disease (PD). PD is a common neurodegenerative disorder causing bradykinesia, resting tremor, muscular rigidity, and postural instability. Cytoplasmic eosinophilic inclusions called Lewy bodies, and neuronal loss especially in the substantia nigra pars compacta, are pathological hallmarks of PD (Valente, E.M. et al (2001) Am. J. Hum. Genet. 68:895-900). Lewy body Parkinson disease has been thought to be a specific autosomal dominant disorder (Wakabayashi, K. et al. (1998) Acta
10 Neuropath. 96:207-210). Juvenile parkinsonism may be a specific autosomal recessive disorder (Matsumine, H. et al. (1997) Am. J. Hum. Genet. 60: 588-596, 1997). (Online Mendelian Inheritance in Man, OMIM. Johns Hopkins University, Baltimore, MD. MIM Number: 168600: Sept. 9, 2002: . World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>)

The discovery of new neurotransmission-associated proteins, and the polynucleotides encoding
15 them, satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of autoimmune/inflammatory disorders, cardiovascular disorders, neurological diseases, developmental disorders, and cell proliferative diseases and disorders, including cancer, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of neurotransmission-associated proteins.

20 There is a need in the art for new compositions, including nucleic acids and proteins, for the diagnosis, prevention, and treatment of autoimmune/inflammatory, cardiovascular, neurological, developmental, cell proliferative, transport, psychiatric, metabolic, and endocrine disorders.

SUMMARY OF THE INVENTION

25 Various embodiments of the invention provide purified polypeptides, neurotransmission-associated proteins, referred to collectively as 'NTRAN' and individually as 'NTRAN-1,' 'NTRAN-2,' 'NTRAN-3,' 'NTRAN-4,' 'NTRAN-5,' 'NTRAN-6,' 'NTRAN-7,' 'NTRAN-8,' 'NTRAN-9,' 'NTRAN-10,' 'NTRAN-11,' 'NTRAN-12,' 'NTRAN-13,' 'NTRAN-14,' 'NTRAN-15,' 'NTRAN-16,' 'NTRAN-17,' 'NTRAN-18,' 'NTRAN-19,' 'NTRAN-20,' 'NTRAN-
30 21,' and 'NTRAN-22' and methods for using these proteins and their encoding polynucleotides for the detection, diagnosis, and treatment of diseases and medical conditions. Embodiments also provide methods for utilizing the purified neurotransmission-associated proteins and/or their encoding

polynucleotides for facilitating the drug discovery process, including determination of efficacy, dosage, toxicity, and pharmacology. Related embodiments provide methods for utilizing the purified neurotransmission-associated proteins and/or their encoding polynucleotides for investigating the pathogenesis of diseases and medical conditions.

5 An embodiment provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected
10 from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. Another embodiment provides an isolated polypeptide comprising an amino acid sequence of SEQ ID NO:1-22.

 Still another embodiment provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the
15 group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group
20 consisting of SEQ ID NO:1-22. In another embodiment, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-22. In an alternative embodiment, the polynucleotide is selected from the group consisting of SEQ ID NO:23-44.

 Still another embodiment provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group
25 consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of
30 a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. Another embodiment provides a cell transformed with the recombinant polynucleotide. Yet another embodiment provides a transgenic organism comprising the recombinant polynucleotide.

Another embodiment provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Yet another embodiment provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

Still yet another embodiment provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In other embodiments, the polynucleotide can comprise at least about 20, 30, 40, 60, 80, or 100 contiguous nucleotides.

Yet another embodiment provides a method for detecting a target polynucleotide in a sample, said target polynucleotide being selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, c) a

polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex. In a related embodiment, the method can include detecting the amount of the hybridization complex. In still other embodiments, the probe can comprise at least about 20, 30, 40, 60, 80, or 100 contiguous nucleotides.

Still yet another embodiment provides a method for detecting a target polynucleotide in a sample, said target polynucleotide being selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof. In a related embodiment, the method can include detecting the amount of the amplified target polynucleotide or fragment thereof.

Another embodiment provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and a pharmaceutically acceptable excipient. In one embodiment, the composition can comprise an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. Other embodiments provide a method of treating a disease or condition associated with decreased or abnormal expression of functional NTRAN, comprising administering to a patient in need of such treatment the composition.

Yet another embodiment provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. Another embodiment provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. Yet another embodiment provides a method of treating a disease or condition associated with decreased expression of functional NTRAN, comprising administering to a patient in need of such treatment the composition.

Still yet another embodiment provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. Another embodiment provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. Yet another embodiment provides a method of treating a disease or condition associated with overexpression of functional NTRAN, comprising administering to a patient in need of such treatment the composition.

Another embodiment provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ

ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the
5 polypeptide.

Yet another embodiment provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical or at least about 90% identical to an
10 amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the
15 polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

20 Still yet another embodiment provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target
25 polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

Another embodiment provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20
30 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at

least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target

5 polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical or at least about 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, iii) a polynucleotide complementary to the polynucleotide of i), iv) a

10 polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide can comprise a fragment of a polynucleotide selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization

15 complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for full length polynucleotide and polypeptide embodiments of the invention.

20 Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog, and the PROTEOME database identification numbers and annotations of PROTEOME database homologs, for polypeptide embodiments of the invention. The probability scores for the matches between each polypeptide and its homolog(s) are also shown.

Table 3 shows structural features of polypeptide embodiments, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the

25 polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide embodiments, along with selected fragments of the polynucleotides.

Table 5 shows representative cDNA libraries for polynucleotide embodiments.

30 Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze polynucleotides and

polypeptides, along with applicable descriptions, references, and threshold parameters.

Table 8 shows single nucleotide polymorphisms found in polynucleotide sequences of the invention, along with allele frequencies in different human populations.

5

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleic acids, and methods are described, it is understood that embodiments of the invention are not limited to the particular machines, instruments, materials, and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the
10 invention.

As used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to “a host cell” includes a plurality of such host cells, and a reference to “an antibody” is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

15

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the
20 cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with various embodiments of the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

“NTRAN” refers to the amino acid sequences of substantially purified NTRAN obtained
25 from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term “agonist” refers to a molecule which intensifies or mimics the biological activity of NTRAN. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of NTRAN either by directly interacting with
30 NTRAN or by acting on components of the biological pathway in which NTRAN participates.

An “allelic variant” is an alternative form of the gene encoding NTRAN. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in

polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times
5 in a given sequence.

“Altered” nucleic acid sequences encoding NTRAN include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as NTRAN or a polypeptide with at least one functional characteristic of NTRAN. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of
10 the polynucleotide encoding NTRAN, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide encoding NTRAN. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent NTRAN. Deliberate amino acid substitutions may be made on the basis of one or more similarities in polarity,
15 charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of NTRAN is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged
20 side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms “amino acid” and “amino acid sequence” can refer to an oligopeptide, a peptide, a polypeptide, or a protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where “amino acid sequence” is recited to refer to a sequence of a naturally
25 occurring protein molecule, “amino acid sequence” and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

“Amplification” relates to the production of additional copies of a nucleic acid. Amplification may be carried out using polymerase chain reaction (PCR) technologies or other nucleic acid amplification technologies well known in the art.

30 The term “antagonist” refers to a molecule which inhibits or attenuates the biological activity of NTRAN. Antagonists may include proteins such as antibodies, anticalins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of

NTRAN either by directly interacting with NTRAN or by acting on components of the biological pathway in which NTRAN participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant.

5 Antibodies that bind NTRAN polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin,
10 thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies
15 which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "aptamer" refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an *in vitro* evolutionary process (e.g., SELEX
20 (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No. 5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a
25 ribonucleotide may be replaced by 2'-F or 2'-NH₂), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system. Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker (Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13).

30 The term "intramer" refers to an aptamer which is expressed *in vivo*. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl. Acad. Sci. USA

96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on
5 substrates containing right-handed nucleotides.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a polynucleotide having a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides
10 having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either
15 transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic NTRAN, or of any oligopeptide
20 thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

25 A "composition comprising a given polynucleotide" and a "composition comprising a given polypeptide" can refer to any composition containing the given polynucleotide or polypeptide. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotides encoding NTRAN or fragments of NTRAN may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as
30 a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

“Consensus sequence” refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (Accelrys, Burlington MA) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

“Conservative amino acid substitutions” are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
15	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
20	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
25	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
30	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A “deletion” refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term “derivative” refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A “detectable label” refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

“Differential expression” refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

“Exon shuffling” refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

A “fragment” is a unique portion of NTRAN or a polynucleotide encoding NTRAN which can be identical in sequence to, but shorter in length than, the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from about 5 to about 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:23-44 can comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:23-44, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:23-44 can be employed in one or more embodiments of methods of the invention, for example, in hybridization and

amplification technologies and in analogous methods that distinguish SEQ ID NO:23-44 from related polynucleotides. The precise length of a fragment of SEQ ID NO:23-44 and the region of SEQ ID NO:23-44 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

5 A fragment of SEQ ID NO:1-22 is encoded by a fragment of SEQ ID NO:23-44. A fragment of SEQ ID NO:1-22 can comprise a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-22. For example, a fragment of SEQ ID NO:1-22 can be used as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-22. The precise length of a fragment of SEQ ID NO:1-22 and the region of SEQ ID NO:1-22 to which
10 the fragment corresponds can be determined based on the intended purpose for the fragment using one or more analytical methods described herein or otherwise known in the art.

A "full length" polynucleotide is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

15 "Homology" refers to sequence similarity or, alternatively, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of identical residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way,
20 gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using one or more computer algorithms or programs known in the art or described herein. For example, percent identity can be determined using the default parameters of the CLUSTAL V algorithm as incorporated into
25 the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989; CABIOS 5:151-153) and in Higgins, D.G. et al. (1992; CABIOS 8:189-191). For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5,
30 window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms which can be used is provided by the National Center for Biotechnology Information (NCBI) Basic

Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of identical residue matches between at least two polypeptide sequences aligned using

a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide. The phrases “percent similarity” and “% similarity,” as applied to polypeptide sequences, refer to the percentage of residue matches, including identical residue matches and conservative substitutions, between at least two polypeptide sequences aligned using a standardized algorithm. In contrast, conservative substitutions are not included in the calculation of percent identity between polypeptide sequences.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62
Open Gap: 11 and Extension Gap: 1 penalties
Gap x drop-off: 50
Expect: 10
Word Size: 3
Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. and D.W. Russell (2001; Molecular Cloning: A Laboratory Manual, 3rd ed., vol. 1-3, Cold Spring Harbor Press, Cold Spring Harbor NY, ch. 9).

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as

formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is
5 strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acids by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid present in solution and another nucleic acid immobilized on a solid support (e.g., paper, membranes, filters, chips,
10 pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or polynucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune
15 disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of NTRAN which is capable of eliciting an immune response when introduced into a living organism, for example, a
20 mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of NTRAN which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, antibodies, or other chemical compounds on a substrate.

25 The terms "element" and "array element" refer to a polynucleotide, polypeptide, antibody, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of NTRAN. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of NTRAN.

30 The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the

antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

“Operably linked” refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding
5 sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs
10 preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

“Post-translational modification” of an NTRAN may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary
15 by cell type depending on the enzymatic milieu of NTRAN.

“Probe” refers to nucleic acids encoding NTRAN, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acids. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. “Primers” are short nucleic
20 acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous
25 nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

30 Methods for preparing and using probes and primers are described in, for example, Sambrook, J. and D.W. Russell (2001; Molecular Cloning: A Laboratory Manual, 3rd ed., vol. 1-3, Cold Spring Harbor Press, Cold Spring Harbor NY), Ausubel, F.M. et al. (1999; Short Protocols in Molecular

Biology, 4th ed., John Wiley & Sons, New York NY), and Innis, M. et al. (1990; PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA). PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

5 Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU
10 primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to
15 avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing
20 selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially
25 complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

 A "recombinant nucleic acid" is a nucleic acid that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly,
30 by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook and Russell (*supra*). The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the

nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA molecule, is composed of the same linear sequence of nucleotides as the reference DNA molecule with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing NTRAN, nucleic acids encoding NTRAN, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably at least about 75% free, and most preferably at least about 90% free from other

components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" or "expression profile" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

10 "Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral
15 infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to animals
20 and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. In another embodiment, the nucleic acid can be introduced by infection with a
25 recombinant viral vector, such as a lentiviral vector (Lois, C. et al. (2002) Science 295:868-872). The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods
30 known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook and Russell (*supra*).

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotides that vary from one species to another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity or sequence similarity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity or sequence similarity over a certain defined length of one of the polypeptides.

THE INVENTION

Various embodiments of the invention include new human neurotransmission-associated proteins (NTRAN), the polynucleotides encoding NTRAN, and the use of these compositions for the diagnosis, treatment, or prevention of autoimmune/inflammatory, cardiovascular, neurological, developmental, cell proliferative, transport, psychiatric, metabolic, and endocrine disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide embodiments of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown. Column 6 shows the Incyte ID numbers of physical, full length clones corresponding to the polypeptide and polynucleotide sequences of the invention. The full length clones encode polypeptides which have at least 95% sequence identity to the polypeptide sequences shown in column 3.

Table 2 shows sequences with homology to polypeptide embodiments of the invention as identified by BLAST analysis against the GenBank protein (genpept) database and the PROTEOME database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (GenBank ID NO:) of the nearest GenBank homolog and the PROTEOME database identification numbers (PROTEOME ID NO:) of the nearest PROTEOME database homologs. Column 4 shows the probability scores for the matches between each polypeptide and its homolog(s). Column 5 shows the annotation of the GenBank and PROTEOME database homolog(s) along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows amino acid residues comprising signature sequences, domains, motifs, potential phosphorylation sites, and potential glycosylation sites. Column 5 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are neurotransmission-associated proteins. For example, For example, SEQ ID NO:5 is 68% identical, from residue E43 to residue D287, and is 60% identical, from residue M1 to G118 to murine gliacolin (GenBank ID g14278927) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability scores are

3.0e-86 and 5.6e-30, which indicate the probabilities of obtaining the observed polypeptide sequence alignments by chance. As determined by BLAST analysis using the PROTEOME database, SEQ ID NO:5 also has homology to murine and human C1q-related factors which have a collagenous region and a globular domain and have similarity to the C1q signature domain. Both murine and human

5 C1q-related factors are highly expressed in brain areas that are involved in motor function (PROTEOME ID 429678|C1qrf and 567880|CRF). SEQ ID NO:5 also contains a C1q domain and a collagen triple helix repeat (20 copies) domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, PROFILESCAN, and additional BLAST

10 analyses provide further corroborative evidence that SEQ ID NO:5 is a C1q-related factor.

In an alternative example, SEQ ID NO:9 is 86% identical, from residue M1 to residue F1308, to Mus musculus cell recognition molecule CASPR4 (GenBank ID g12330704) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance.

15 SEQ ID NO:9 also has homology to Neurexin 4 (contactin associated protein 1), a neuronal paranodal transmembrane receptor containing epidermal growth factor-like and neurexin motifs, as determined by BLAST analysis using the PROTEOME database. SEQ ID NO:9 also contains an EGF-like domain and a F5/8 type C domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See

20 Table 3.) Data from BLIMPS and MOTIFS analyses provide further corroborative evidence that SEQ ID NO:9 is a cell recognition molecule.

In an alternative example, SEQ ID NO:13 is 100% identical, from residue M1 to residue S573, to human myelin-associated glycoprotein precursor (GenBank ID g307156) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0,

25 which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:13 also has homology to proteins that are localized to the nervous system, are members of the sialoadhesin subgroup of immunoglobulin superfamily lectins, and are cell adhesion molecules, as determined by BLAST analysis using the PROTEOME database. SEQ ID NO:13 also contains an I-type IG domain, an Immunoglobulin domain, an Ig superfamily from SCOP domain and an

30 Immunoglobulin C-2 type domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM, INCY and SMART databases of conserved protein families/domains. (See Table 3.) Data from BLIMPS, MOTIFS, and additional BLAST analyses

provide further corroborative evidence that SEQ ID NO:13 is a myelin cell adhesion molecule.

In an alternative example, SEQ ID NO:16 is 93% identical, from residue A32 to residue S412, to human ubiquilin (GenBank ID g18254511) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $4.6e-185$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:16 also has homology to proteins that are localized to the endoplasmic reticulum, nucleus, and cytoplasm, is associated with the 26S proteasome, binds to and promotes the accumulation of presenilin 1 and presenilin 2, and are localized to neurofibrillary tangles and Lewy bodies in brains affected by Alzheimer's disease and Parkinson's disease, and are annotated as ubiquilin 1 proteins, as determined by BLAST analysis using the PROTEOME database. SEQ ID NO:16 also contains UBA/TS-N and ubiquitin associated domains as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM and SMART database of conserved protein families/domains. (See Table 3.) Data from BLAST analyses against the PRODOM database, provide further corroborative evidence that SEQ ID NO:16 is a ubiquilin protein.

In an alternative example, SEQ ID NO:19 is 89% identical, from residue M1 to residue L621, to *Mus musculus* punc (g3068592) as determined by the Basic Local Alignment Search Tool (BLAST). The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:19 also has homology to proteins that are localized to the plasma membrane, are members of the immunoglobulin superfamily, and are neuronal cell adhesion proteins, as determined by BLAST analysis using the PROTEOME database. SEQ ID NO:19 also contains fibronectin type 3 and immunoglobulin domains as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM, INCY, and SMART databases of conserved protein families/domains. (See Table 3.) Data from BLAST analyses against the PRODOM and DOMO databases, provide further corroborative evidence that SEQ ID NO:19 is a neuronal cell adhesion protein.

SEQ ID NO:1-4, SEQ ID NO:6-8, SEQ ID NO:10-12, SEQ ID NO:14-15, SEQ ID NO:17-18, and SEQ ID NO:20-22 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-22 are described in Table 7.

As shown in Table 4, the full length polynucleotide embodiments were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Column 1 lists the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:), the corresponding Incyte polynucleotide consensus sequence number (Incyte ID) for

each polynucleotide of the invention, and the length of each polynucleotide sequence in basepairs. Column 2 shows the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences used to assemble the full length polynucleotide embodiments, and of fragments of the polynucleotides which are useful, for example, in hybridization or amplification technologies that
 5 identify SEQ ID NO:23-44 or that distinguish between SEQ ID NO:23-44 and related polynucleotides.

The polynucleotide fragments described in Column 2 of Table 4 may refer specifically, for example, to Incyte cDNAs derived from tissue-specific cDNA libraries or from pooled cDNA libraries. Alternatively, the polynucleotide fragments described in column 2 may refer to GenBank cDNAs or ESTs which contributed to the assembly of the full length polynucleotides. In addition, the
 10 polynucleotide fragments described in column 2 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences including the designation "ENST"). Alternatively, the polynucleotide fragments described in column 2 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including the designation "NM" or "NT") or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences
 15 including the designation "NP"). Alternatively, the polynucleotide fragments described in column 2 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. For example, a polynucleotide sequence identified as FL_XXXXXX_N₁_N₂_YYYYY_N₃_N₄ represents a "stitched" sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYYY is the
 20 number of the prediction generated by the algorithm, and N_{1,2,3...}, if present, represent specific exons that may have been manually edited during analysis (See Example V). Alternatively, the polynucleotide fragments in column 2 may refer to assemblages of exons brought together by an "exon-stretching" algorithm. For example, a polynucleotide sequence identified as FLXXXXXX_gAAAAA_gBBBBB_1_N is a "stretched" sequence, with XXXXXX being the Incyte project identification number, gAAAAA being the GenBank identification number of the human
 25 genomic sequence to which the "exon-stretching" algorithm was applied, gBBBBB being the GenBank identification number or NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to specific exons (See Example V). In instances where a RefSeq sequence was used as a protein homolog for the "exon-stretching" algorithm, a RefSeq identifier (denoted by "NM,"
 30 "NP," or "NT") may be used in place of the GenBank identifier (*i.e.*, gBBBBB).

Alternatively, a prefix identifies component sequences that were hand-edited, predicted from genomic DNA sequences, or derived from a combination of sequence analysis methods. The

following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK).
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).
INCY	Full length transcript and exon prediction from mapping of EST sequences to the genome. Genomic location and EST composition data are combined to predict the exons and resulting transcript.

In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in Table 4 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotides which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotides. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

Table 8 shows single nucleotide polymorphisms (SNPs) found in polynucleotide sequences of the invention, along with allele frequencies in different human populations. Columns 1 and 2 show the polynucleotide sequence identification number (SEQ ID NO:) and the corresponding Incyte project identification number (PID) for polynucleotides of the invention. Column 3 shows the Incyte identification number for the EST in which the SNP was detected (EST ID), and column 4 shows the identification number for the SNP (SNP ID). Column 5 shows the position within the EST sequence at which the SNP is located (EST SNP), and column 6 shows the position of the SNP within the full-length polynucleotide sequence (CB1 SNP). Column 7 shows the allele found in the EST sequence. Columns 8 and 9 show the two alleles found at the SNP site. Column 10 shows the amino acid encoded by the codon including the SNP site, based upon the allele found in the EST. Columns 11-14 show the frequency of allele 1 in four different human populations. An entry of n/d (not detected) indicates that the frequency of allele 1 in the population was too low to be detected, while n/a (not

available) indicates that the allele frequency was not determined for the population.

The invention also encompasses NTRAN variants. Various embodiments of NTRAN variants can have at least about 80%, at least about 90%, or at least about 95% amino acid sequence identity to the NTRAN amino acid sequence, and can contain at least one functional or structural characteristic of NTRAN.

Various embodiments also encompass polynucleotides which encode NTRAN. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:23-44, which encodes NTRAN. The polynucleotide sequences of SEQ ID NO:23-44, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses variants of a polynucleotide encoding NTRAN. In particular, such a variant polynucleotide will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a polynucleotide encoding NTRAN. A particular aspect of the invention encompasses a variant of a polynucleotide comprising a sequence selected from the group consisting of SEQ ID NO:23-44 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:23-44. Any one of the polynucleotide variants described above can encode a polypeptide which contains at least one functional or structural characteristic of NTRAN.

In addition, or in the alternative, a polynucleotide variant of the invention is a splice variant of a polynucleotide encoding NTRAN. A splice variant may have portions which have significant sequence identity to a polynucleotide encoding NTRAN, but will generally have a greater or lesser number of polynucleotides due to additions or deletions of blocks of sequence arising from alternate splicing of exons during mRNA processing. A splice variant may have less than about 70%, or alternatively less than about 60%, or alternatively less than about 50% polynucleotide sequence identity to a polynucleotide encoding NTRAN over its entire length; however, portions of the splice variant will have at least about 70%, or alternatively at least about 85%, or alternatively at least about 95%, or alternatively 100% polynucleotide sequence identity to portions of the polynucleotide encoding NTRAN. For example, a polynucleotide comprising a sequence of SEQ ID NO:33 and a polynucleotide comprising a sequence of SEQ ID NO:34 are splice variants of each other. Any one of the splice variants described above can encode a polypeptide which contains at least one functional

or structural characteristic of NTRAN.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding NTRAN, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring NTRAN, and all such variations are to be considered as being specifically disclosed.

Although polynucleotides which encode NTRAN and its variants are generally capable of hybridizing to polynucleotides encoding naturally occurring NTRAN under appropriately selected conditions of stringency, it may be advantageous to produce polynucleotides encoding NTRAN or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding NTRAN and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of polynucleotides which encode NTRAN and NTRAN derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic polynucleotide may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a polynucleotide encoding NTRAN or any fragment thereof.

Embodiments of the invention can also include polynucleotides that are capable of hybridizing to the claimed polynucleotides, and, in particular, to those having the sequences shown in SEQ ID NO:23-44 and fragments thereof, under various conditions of stringency (Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511). Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied

Biosystems), thermostable T7 polymerase (Amersham Biosciences, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Invitrogen, Carlsbad CA). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cyclers (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cyclers (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Amersham Biosciences), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art (Ausubel et al., *supra*, ch. 7; Meyers, R.A. (1995) Molecular Biology and
10 Biotechnology, Wiley VCH, New York NY, pp. 856-853).

The nucleic acids encoding NTRAN may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a
15 cloning vector (Sarkar, G. (1993) PCR Methods Appl. 2:318-322). Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and
20 yeast artificial chromosome DNA (Lagerstrom, M. et al. (1991) PCR Methods Appl. 1:111-119). In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art (Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and
25 PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the
30 template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include

sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotides or fragments thereof which encode NTRAN may be cloned in recombinant DNA molecules that direct expression of NTRAN, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other polynucleotides which encode substantially the same or a functionally equivalent polypeptides may be produced and used to express NTRAN.

The polynucleotides of the invention can be engineered using methods generally known in the art in order to alter NTRAN-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent No. 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of NTRAN, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These

preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, 5 fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, polynucleotides encoding NTRAN may be synthesized, in whole or in part, using one or more chemical methods well known in the art (Caruthers, M.H. et al. (1980) 10 Nucleic Acids Symp. Ser. 7:215-223; Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232). Alternatively, NTRAN itself or a fragment thereof may be synthesized using chemical methods known in the art. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques (Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; Roberge, J.Y. et al. (1995) Science 269:202-204). Automated 15 synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of NTRAN, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid 20 chromatography (Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421). The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing (Creighton, *supra*, pp. 28-53).

In order to express a biologically active NTRAN, the polynucleotides encoding NTRAN or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains 25 the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotides encoding NTRAN. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of polynucleotides encoding NTRAN. Such signals 30 include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where a polynucleotide sequence encoding NTRAN and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control

signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used (Scharf, D. et al. (1994) Results Probl. Cell Differ. 20:125-162).

Methods which are well known to those skilled in the art may be used to construct expression vectors containing polynucleotides encoding NTRAN and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination (Sambrook and Russell, *supra*, ch. 1-4, and 8; Ausubel et al., *supra*, ch. 1, 3, and 15).

A variety of expression vector/host systems may be utilized to contain and express polynucleotides encoding NTRAN. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems (Sambrook and Russell, *supra*; Ausubel et al., *supra*; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355). Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of polynucleotides to the targeted organ, tissue, or cell population (Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5:350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Buller, R.M. et al. (1985) Nature 317:813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31:219-226; Verma, I.M. and N. Somia (1997) Nature 389:239-242). The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotides encoding NTRAN. For example, routine cloning, subcloning, and propagation of polynucleotides encoding NTRAN can be achieved using a

multifunctional *E. coli* vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Invitrogen). Ligation of polynucleotides encoding NTRAN into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for

5 *in vitro* transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence (Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509). When large quantities of NTRAN are needed, e.g. for the production of antibodies, vectors which direct high level expression of NTRAN may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

10 Yeast expression systems may be used for production of NTRAN. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign polynucleotide sequences into the host genome for stable propagation (Ausubel et al.,

15 *supra*; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184).

Plant systems may also be used for expression of NTRAN. Transcription of polynucleotides encoding NTRAN may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.*

20 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection (The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp.

25 191-196).

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, polynucleotides encoding NTRAN may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to

30 obtain infective virus which expresses NTRAN in host cells (Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-

based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes (Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355).

For long term production of recombinant proteins in mammalian systems, stable expression of NTRAN in cell lines is preferred. For example, polynucleotides encoding NTRAN can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* and *ap^r* cells, respectively (Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823). Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14). Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites (Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051). Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β -glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding NTRAN is inserted within a marker gene sequence, transformed cells

containing polynucleotides encoding NTRAN can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding NTRAN under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

5 In general, host cells that contain the polynucleotide encoding NTRAN and that express NTRAN may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

10 Immunological methods for detecting and measuring the expression of NTRAN using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on NTRAN is preferred, but a
15 competitive binding assay may be employed. These and other assays are well known in the art (Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ).

20 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding NTRAN include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, polynucleotides encoding NTRAN, or any fragments thereof, may be cloned into a
25 vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Biosciences, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be
30 used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with polynucleotides encoding NTRAN may be cultured under

conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode NTRAN may be designed to contain signal sequences which direct
5 secretion of NTRAN through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted polynucleotides or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a “prepro” or
10 “pro” form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

15 In another embodiment of the invention, natural, modified, or recombinant polynucleotides encoding NTRAN may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric NTRAN protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of NTRAN activity. Heterologous protein and
20 peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins,
25 respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the NTRAN encoding sequence and the heterologous protein sequence, so that NTRAN may be cleaved away from the heterologous moiety following purification. Methods for
30 fusion protein expression and purification are discussed in Ausubel et al. (*supra*, ch. 10 and 16). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In another embodiment, synthesis of radiolabeled NTRAN may be achieved *in vitro* using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

NTRAN, fragments of NTRAN, or variants of NTRAN may be used to screen for compounds that specifically bind to NTRAN. One or more test compounds may be screened for specific binding to NTRAN. In various embodiments, 1, 2, 3, 4, 5, 10, 20, 50, 100, or 200 test compounds can be screened for specific binding to NTRAN. Examples of test compounds can include antibodies, anticalins, oligonucleotides, proteins (e.g., ligands or receptors), or small molecules.

In related embodiments, variants of NTRAN can be used to screen for binding of test compounds, such as antibodies, to NTRAN, a variant of NTRAN, or a combination of NTRAN and/or one or more variants NTRAN. In an embodiment, a variant of NTRAN can be used to screen for compounds that bind to a variant of NTRAN, but not to NTRAN having the exact sequence of a sequence of SEQ ID NO:1-22. NTRAN variants used to perform such screening can have a range of about 50% to about 99% sequence identity to NTRAN, with various embodiments having 60%, 70%, 75%, 80%, 85%, 90%, and 95% sequence identity.

In an embodiment, a compound identified in a screen for specific binding to NTRAN can be closely related to the natural ligand of NTRAN, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner (Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2):Chapter 5). In another embodiment, the compound thus identified can be a natural ligand of a receptor NTRAN (Howard, A.D. et al. (2001) Trends Pharmacol. Sci.22:132-140; Wise, A. et al. (2002) Drug Discovery Today 7:235-246).

In other embodiments, a compound identified in a screen for specific binding to NTRAN can be closely related to the natural receptor to which NTRAN binds, at least a fragment of the receptor, or a fragment of the receptor including all or a portion of the ligand binding site or binding pocket. For example, the compound may be a receptor for NTRAN which is capable of propagating a signal, or a decoy receptor for NTRAN which is not capable of propagating a signal (Ashkenazi, A. and V.M. Divit (1999) Curr. Opin. Cell Biol. 11:255-260; Mantovani, A. et al. (2001) Trends Immunol. 22:328-336). The compound can be rationally designed using known techniques. Examples of such techniques include those used to construct the compound etanercept (ENBREL; Amgen Inc., Thousand Oaks CA), which is efficacious for treating rheumatoid arthritis in humans. Etanercept is

an engineered p75 tumor necrosis factor (TNF) receptor dimer linked to the Fc portion of human IgG₁ (Taylor, P.C. et al. (2001) Curr. Opin. Immunol. 13:611-616).

In one embodiment, two or more antibodies having similar or, alternatively, different specificities can be screened for specific binding to NTRAN, fragments of NTRAN, or variants of NTRAN. The binding specificity of the antibodies thus screened can thereby be selected to identify particular fragments or variants of NTRAN. In one embodiment, an antibody can be selected such that its binding specificity allows for preferential identification of specific fragments or variants of NTRAN. In another embodiment, an antibody can be selected such that its binding specificity allows for preferential diagnosis of a specific disease or condition having increased, decreased, or otherwise abnormal production of NTRAN.

In an embodiment, anticalins can be screened for specific binding to NTRAN, fragments of NTRAN, or variants of NTRAN. Anticalins are ligand-binding proteins that have been constructed based on a lipocalin scaffold (Weiss, G.A. and H.B. Lowman (2000) Chem. Biol. 7:R177-R184; Skerra, A. (2001) J. Biotechnol. 74:257-275). The protein architecture of lipocalins can include a beta-barrel having eight antiparallel beta-strands, which supports four loops at its open end. These loops form the natural ligand-binding site of the lipocalins, a site which can be re-engineered *in vitro* by amino acid substitutions to impart novel binding specificities. The amino acid substitutions can be made using methods known in the art or described herein, and can include conservative substitutions (e.g., substitutions that do not alter binding specificity) or substitutions that modestly, moderately, or significantly alter binding specificity.

In one embodiment, screening for compounds which specifically bind to, stimulate, or inhibit NTRAN involves producing appropriate cells which express NTRAN, either as a secreted protein or on the cell membrane. Preferred cells can include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing NTRAN or cell membrane fractions which contain NTRAN are then contacted with a test compound and binding, stimulation, or inhibition of activity of either NTRAN or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with NTRAN, either in solution or affixed to a solid support, and detecting the binding of NTRAN to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical

libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

An assay can be used to assess the ability of a compound to bind to its natural ligand and/or to inhibit the binding of its natural ligand to its natural receptors. Examples of such assays include radio-labeling assays such as those described in U.S. Patent No. 5,914,236 and U.S. Patent No. 6,372,724. In a related embodiment, one or more amino acid substitutions can be introduced into a polypeptide compound (such as a receptor) to improve or alter its ability to bind to its natural ligands (Matthews, D.J. and J.A. Wells. (1994) Chem. Biol. 1:25-30). In another related embodiment, one or more amino acid substitutions can be introduced into a polypeptide compound (such as a ligand) to improve or alter its ability to bind to its natural receptors (Cunningham, B.C. and J.A. Wells (1991) Proc. Natl. Acad. Sci. USA 88:3407-3411; Lowman, H.B. et al. (1991) J. Biol. Chem. 266:10982-10988).

NTRAN, fragments of NTRAN, or variants of NTRAN may be used to screen for compounds that modulate the activity of NTRAN. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for NTRAN activity, wherein NTRAN is combined with at least one test compound, and the activity of NTRAN in the presence of a test compound is compared with the activity of NTRAN in the absence of the test compound. A change in the activity of NTRAN in the presence of the test compound is indicative of a compound that modulates the activity of NTRAN. Alternatively, a test compound is combined with an *in vitro* or cell-free system comprising NTRAN under conditions suitable for NTRAN activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of NTRAN may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding NTRAN or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease (see, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337). For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (*neo*; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D.

(1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330).

Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding NTRAN may also be manipulated *in vitro* in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding NTRAN can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding NTRAN is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress NTRAN, e.g., by secreting NTRAN in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of NTRAN and neurotransmission-associated proteins. In addition, examples of tissues expressing NTRAN can be found in Table 6 and can also be found in Example XI. Therefore, NTRAN appears to play a role in autoimmune/inflammatory, cardiovascular, neurological, developmental, cell proliferative, transport, psychiatric, metabolic, and endocrine disorders. In the treatment of disorders associated with increased NTRAN expression or activity, it is desirable to decrease the expression or activity of NTRAN. In the treatment of disorders associated with decreased NTRAN expression or activity, it is desirable to increase the expression or activity of NTRAN.

Therefore, in one embodiment, NTRAN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NTRAN. Examples of such disorders include, but are not limited to, an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's

disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic

5 lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thromb osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome,

10 rheumatoid arthritis, scleroderma, Sjögren's ocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a cardiovascular disorder such as congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid

15 aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose

20 veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy,

25 retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous

30 sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord

diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive

5 dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome,

10 myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,

15 hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, colon, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid,

20 penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus and a cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; a transport disorder such as

25 akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral

30 neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol

myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy,

5 sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease; a psychiatric disorder such

10 as acute stress disorder, alcohol dependence, amphetamine dependence, anorexia nervosa, antisocial personality disorder, attention-deficit hyperactivity disorder, autistic disorder, anxiety, avoidant personality disorder, bipolar disorder, borderline personality disorder, brief psychotic disorder, bulimia nervosa, cannabis dependence, cocaine dependence, conduct disorder, cyclothymic disorder, delirium, delusional disorder, dementia, dependent personality disorder, depression, dysthymic disorder,

15 hallucinogen dependence, histrionic personality disorder, inhalant dependence, manic depression, multi-infarct dementia, narcissistic personality disorder, nicotine dependence, obsessive-compulsive disorder, opioid dependence, oppositional defiant disorder, panic disorder, paranoid personality disorder, phencyclidine dependence, phobia, posttraumatic stress disorder, schizoaffective disorder, schizoid personality disorder, schizophrenia, sedative dependence, separation anxiety disorder, and sleep

20 disorder; a metabolic disorder such as Addison's disease, cerebrotendinous xanthomatosis, congenital adrenal hyperplasia, coumarin resistance, cystic fibrosis, fatty hepatocirrhosis, fructose-1,6-diphosphatase deficiency, galactosemia, goiter, glucagonoma, glycogen storage diseases, hereditary fructose intolerance, hyperadrenalism, hypoadrenalism, hyperparathyroidism, hypoparathyroidism, hypercholesterolemia, hyperthyroidism, hypoglycemia, hypothyroidism,

25 hyperlipidemia, hyperlipemia, lipid myopathies, lipodystrophies, lysosomal storage diseases, mannosidosis, neuraminidase deficiency, obesity, osteoporosis, phenylketonuria, pseudovitamin D-deficiency rickets, disorders of carbohydrate metabolism such as congenital type II dyserythropoietic anemia, diabetes, insulin-dependent diabetes mellitus, non-insulin-dependent diabetes mellitus, galactose epimerase deficiency, glycogen storage diseases, lysosomal storage diseases, fructosuria,

30 pentosuria, and inherited abnormalities of pyruvate metabolism, disorders of lipid metabolism such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such

Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis,

5 hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, and lipid myopathies, and disorders of copper metabolism such as Menke's disease, Wilson's disease, and Ehlers-Danlos syndrome type IX

10 diabetes; and an endocrine disorder such as a disorder of the hypothalamus and/or pituitary resulting from lesions such as a primary brain tumor, adenoma, infarction associated with pregnancy, hypophysectomy, aneurysm, vascular malformation, thrombosis, infection, immunological disorder, and complication due to head trauma, a disorder associated with hypopituitarism including hypogonadism, Sheehan syndrome, diabetes insipidus, Kallman's disease, Hand-Schuller-Christian disease, Letterer-

15 Siwe disease, sarcoidosis, empty sella syndrome, and dwarfism, a disorder associated with hyperpituitarism including acromegaly, gigantism, and syndrome of inappropriate antidiuretic hormone (ADH) secretion (SIADH) often caused by benign adenoma, a disorder associated with hypothyroidism including goiter, myxedema, acute thyroiditis associated with bacterial infection, subacute thyroiditis associated with viral infection, autoimmune thyroiditis (Hashimoto's disease), and

20 cretinism, a disorder associated with hyperthyroidism including thyrotoxicosis and its various forms, Grave's disease, pretibial myxedema, toxic multinodular goiter, thyroid carcinoma, and Plummer's disease, a disorder associated with hyperparathyroidism including Conn disease (chronic hypercalcemia), a pancreatic disorder such as Type I or Type II diabetes mellitus and associated complications, a disorder associated with the adrenals such as hyperplasia, carcinoma, or adenoma of

25 the adrenal cortex, hypertension associated with alkalosis, amyloidosis, hypokalemia, Cushing's disease, Liddle's syndrome, and Arnold-Healy-Gordon syndrome, pheochromocytoma tumors, and Addison's disease, a disorder associated with gonadal steroid hormones such as: in women, abnormal prolactin production, infertility, endometriosis, perturbation of the menstrual cycle, polycystic ovarian disease, hyperprolactinemia, isolated gonadotropin deficiency, amenorrhea, galactorrhea,

30 hermaphroditism, hirsutism and virilization, breast cancer, and, in post-menopausal women, osteoporosis, and, in men, Leydig cell deficiency, male climacteric phase, and germinal cell aplasia, a hypergonadal disorder associated with Leydig cell tumors, androgen resistance associated with

absence of androgen receptors, syndrome of 5 α -reductase, and gynecomastia.

In another embodiment, a vector capable of expressing NTRAN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NTRAN including, but not limited to, those described above.

5 In a further embodiment, a composition comprising a substantially purified NTRAN in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NTRAN including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of NTRAN may be
10 administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NTRAN including, but not limited to, those listed above.

In a further embodiment, an antagonist of NTRAN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of NTRAN. Examples of such disorders include, but are not limited to, those autoimmune/inflammatory, cardiovascular, neurological,
15 developmental, cell proliferative, transport, psychiatric, metabolic, and endocrine disorders described above. In one aspect, an antibody which specifically binds NTRAN may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express NTRAN.

In an additional embodiment, a vector expressing the complement of the polynucleotide
20 encoding NTRAN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of NTRAN including, but not limited to, those described above.

In other embodiments, any protein, agonist, antagonist, antibody, complementary sequence, or vector embodiments may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary
25 skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of NTRAN may be produced using methods which are generally known in the
30 art. In particular, purified NTRAN may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind NTRAN. Antibodies to NTRAN may also be generated using methods that are well known in the art. Such antibodies may include, but are

not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. In an embodiment, neutralizing antibodies (i.e., those which inhibit dimer formation) can be used therapeutically. Single chain antibodies (e.g., from camels or llamas) may be potent enzyme inhibitors and may have application in the design of peptide mimetics, and in the development of immuno-adsorbents and biosensors (Muyldermans, S. (2001) J. Biotechnol. 74:277-302).

For the production of antibodies, various hosts including goats, rabbits, rats, mice, camels, dromedaries, llamas, humans, and others may be immunized by injection with NTRAN or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum* are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to NTRAN have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are substantially identical to a portion of the amino acid sequence of the natural protein. Short stretches of NTRAN amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to NTRAN may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120).

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; Takeda, S. et al. (1985) Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce NTRAN-specific single chain antibodies.

Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries (Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137).

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population
5 or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299).

Antibody fragments which contain specific binding sites for NTRAN may also be generated. For example, such fragments include, but are not limited to, $F(ab)_2$ fragments produced by pepsin
10 digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the $F(ab)_2$ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse, W.D. et al. (1989) Science 246:1275-1281).

Various immunoassays may be used for screening to identify antibodies having the desired
15 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between NTRAN and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering NTRAN epitopes is generally used, but a competitive binding assay may also be
20 employed (Pound, *supra*).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for NTRAN. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of NTRAN-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a
25 determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple NTRAN epitopes, represents the average affinity, or avidity, of the antibodies for NTRAN. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular NTRAN epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the NTRAN-
30 antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of NTRAN, preferably in active form, from the

antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of NTRAN-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available (Catty, *supra*; Coligan et al., *supra*).

In another embodiment of the invention, polynucleotides encoding NTRAN, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding NTRAN. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding NTRAN (Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press, Totawa NJ).

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein (Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102:469-475; Scanlon, K.J. et al. (1995) 9:1288-1296). Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors (Miller, A.D. (1990) *Blood* 76:271; Ausubel et al., *supra*; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63:323-347). Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art (Rossi, J.J. (1995) *Br. Med. Bull.* 51:217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87:1308-1315; Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25:2730-2736).

In another embodiment of the invention, polynucleotides encoding NTRAN may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined

immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassamias, familial
 5 hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988)
 10 Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as *Candida albicans* and *Paracoccidioides brasiliensis*; and protozoan parasites such as *Plasmodium falciparum* and *Trypanosoma cruzi*). In the case where a genetic deficiency in NTRAN expression or regulation causes disease, the expression of NTRAN from an appropriate population of transduced cells may alleviate the clinical
 15 manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in NTRAN are treated by constructing mammalian expression vectors encoding NTRAN and introducing these vectors by mechanical means into NTRAN-deficient cells. Mechanical transfer technologies for use with cells *in vivo* or *ex vitro* include (i) direct DNA microinjection into individual
 20 cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J.-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of NTRAN include, but are not
 25 limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX, PCR2-TOPOTA vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). NTRAN may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter
 30 (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen));

the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and H.M. Blau, *supra*), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding NTRAN from a normal individual.

5 Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al.
10 (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

 In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to NTRAN expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding NTRAN under the control of an independent promoter or the retrovirus long
15 terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in
20 an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent No. 5,910,434 to Rigg ("Method for obtaining
25 retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).
30

 In an embodiment, an adenovirus-based gene therapy delivery system is used to deliver

polynucleotides encoding NTRAN to cells which have one or more genetic abnormalities with respect to the expression of NTRAN. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas
5 (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent No. 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999; Annu. Rev. Nutr. 19:511-544) and Verma, I.M. and N. Somia (1997; Nature 18:389:239-242).

In another embodiment, a herpes-based, gene therapy delivery system is used to deliver
10 polynucleotides encoding NTRAN to target cells which have one or more genetic abnormalities with respect to the expression of NTRAN. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing NTRAN to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has
15 been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent No. 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent No. 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under
20 the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999; J. Virol. 73:519-532) and Xu, H. et al. (1994; Dev. Biol. 163:152-161). The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the
25 large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another embodiment, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding NTRAN to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based
30 on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA,

resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for NTRAN into the alphavirus genome in place of the capsid-coding region results in the production of a large number of NTRAN-coding RNAs and the synthesis of high levels of NTRAN in vector transduced cells. While
5 alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of NTRAN into a variety of cell types. The specific transduction of a subset of
10 cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10
15 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature (Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and
20 Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177). A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme
25 molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of RNA molecules encoding NTRAN.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA,
30 GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of

candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA molecules encoding NTRAN. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

In other embodiments of the invention, the expression of one or more selected polynucleotides of the present invention can be altered, inhibited, decreased, or silenced using RNA interference (RNAi) or post-transcriptional gene silencing (PTGS) methods known in the art. RNAi is a post-transcriptional mode of gene silencing in which double-stranded RNA (dsRNA) introduced into a targeted cell specifically suppresses the expression of the homologous gene (i.e., the gene bearing the sequence complementary to the dsRNA). This effectively knocks out or substantially reduces the expression of the targeted gene. PTGS can also be accomplished by use of DNA or DNA fragments as well. RNAi methods are described by Fire, A. et al. (1998; Nature 391:806-811) and Gura, T. (2000; Nature 404:804-808). PTGS can also be initiated by introduction of a complementary segment of DNA into the selected tissue using gene delivery and/or viral vector delivery methods described herein or known in the art.

RNAi can be induced in mammalian cells by the use of small interfering RNA also known as siRNA. SiRNA are shorter segments of dsRNA (typically about 21 to 23 nucleotides in length) that result *in vivo* from cleavage of introduced dsRNA by the action of an endogenous ribonuclease. SiRNA appear to be the mediators of the RNAi effect in mammals. The most effective siRNAs

appear to be 21 nucleotide dsRNAs with 2 nucleotide 3' overhangs. The use of siRNA for inducing RNAi in mammalian cells is described by Elbashir, S.M. et al. (2001; Nature 411:494-498).

SiRNA can either be generated indirectly by introduction of dsRNA into the targeted cell, or directly by mammalian transfection methods and agents described herein or known in the art (such as liposome-mediated transfection, viral vector methods, or other polynucleotide delivery/introductory methods). Suitable SiRNAs can be selected by examining a transcript of the target polynucleotide (e.g., mRNA) for nucleotide sequences downstream from the AUG start codon and recording the occurrence of each nucleotide and the 3' adjacent 19 to 23 nucleotides as potential siRNA target sites, with sequences having a 21 nucleotide length being preferred. Regions to be avoided for target siRNA sites include the 5' and 3' untranslated regions (UTRs) and regions near the start codon (within 75 bases), as these may be richer in regulatory protein binding sites. UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP endonuclease complex. The selected target sites for siRNA can then be compared to the appropriate genome database (e.g., human, etc.) using BLAST or other sequence comparison algorithms known in the art. Target sequences with significant homology to other coding sequences can be eliminated from consideration. The selected SiRNAs can be produced by chemical synthesis methods known in the art or by *in vitro* transcription using commercially available methods and kits such as the SILENCER siRNA construction kit (Ambion, Austin TX).

In alternative embodiments, long-term gene silencing and/or RNAi effects can be induced in selected tissue using expression vectors that continuously express siRNA. This can be accomplished using expression vectors that are engineered to express hairpin RNAs (shRNAs) using methods known in the art (see, e.g., Brummelkamp, T.R. et al. (2002) Science 296:550-553; and Paddison, P.J. et al. (2002) Genes Dev. 16:948-958). In these and related embodiments, shRNAs can be delivered to target cells using expression vectors known in the art. An example of a suitable expression vector for delivery of siRNA is the PSILENCER1.0-U6 (circular) plasmid (Ambion). Once delivered to the target tissue, shRNAs are processed *in vivo* into siRNA-like molecules capable of carrying out gene-specific silencing.

In various embodiments, the expression levels of genes targeted by RNAi or PTGS methods can be determined by assays for mRNA and/or protein analysis. Expression levels of the mRNA of a targeted gene, can be determined by northern analysis methods using, for example, the NORTHERNMAX-GLY kit (Ambion); by microarray methods; by PCR methods; by real time PCR methods; and by other RNA/polynucleotide assays known in the art or described herein. Expression

levels of the protein encoded by the targeted gene can be determined by Western analysis using standard techniques known in the art.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding NTRAN.

5 Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of
10 polynucleotide expression. Thus, in the treatment of disorders associated with increased NTRAN expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding NTRAN may be therapeutically useful, and in the treatment of disorders associated with decreased NTRAN expression or activity, a compound which specifically promotes expression of the polynucleotide encoding NTRAN may be therapeutically useful.

15 In various embodiments, one or more test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound
20 based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding NTRAN is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an *in vitro* cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding NTRAN are assayed
25 by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding NTRAN. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to
30 a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a *Schizosaccharomyces pombe* gene expression system

(Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use *in vivo*, *in vitro*, and *ex vivo*. For *ex vivo* therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art (Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466).

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of NTRAN, antibodies to NTRAN, and mimetics, agonists, antagonists, or inhibitors of NTRAN.

In various embodiments, the compositions described herein, such as pharmaceutical compositions, may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S.

et al., U.S. Patent No. 5,997,848). Pulmonary delivery allows administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination
5 of an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising NTRAN or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, NTRAN or a fragment thereof may be joined to a short cationic N-
10 terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys,
15 or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example NTRAN or fragments thereof, antibodies of NTRAN, and agonists, antagonists or inhibitors of
20 NTRAN, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large
25 therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

30 The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the

severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

5 Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells,
10 conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind NTRAN may be used for the diagnosis of disorders characterized by expression of NTRAN, or in assays to monitor patients being treated with NTRAN or agonists, antagonists, or inhibitors of NTRAN. Antibodies useful for
15 diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for NTRAN include methods which utilize the antibody and a label to detect NTRAN in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in
20 the art and may be used.

A variety of protocols for measuring NTRAN, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of NTRAN expression. Normal or standard values for NTRAN expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to
25 NTRAN under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of NTRAN expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, polynucleotides encoding NTRAN may be used for
30 diagnostic purposes. The polynucleotides which may be used include oligonucleotides, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of NTRAN may be correlated with disease. The

diagnostic assay may be used to determine absence, presence, and excess expression of NTRAN, and to monitor regulation of NTRAN levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotides, including genomic sequences, encoding NTRAN or closely related molecules may be used to identify
5 nucleic acid sequences which encode NTRAN. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding NTRAN, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50%
10 sequence identity to any of the NTRAN encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:23-44 or from genomic sequences including promoters, enhancers, and introns of the NTRAN gene.

Means for producing specific hybridization probes for polynucleotides encoding NTRAN include the cloning of polynucleotides encoding NTRAN or NTRAN derivatives into vectors for the
15 production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

20 Polynucleotides encoding NTRAN may be used for the diagnosis of disorders associated with expression of NTRAN. Examples of such disorders include, but are not limited to, an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune
25 polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or
30 pericardial inflammation, syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thromb osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's ocytopenic purpura, ulcerative colitis, uveitis, Werner

syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a cardiovascular disorder such as congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary

neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, colon, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus and a cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease; a psychiatric disorder such as acute stress disorder, alcohol dependence, amphetamine dependence, anorexia nervosa, antisocial

personality disorder, attention-deficit hyperactivity disorder, autistic disorder, anxiety, avoidant
 personality disorder, bipolar disorder, borderline personality disorder, brief psychotic disorder, bulimia
 nervosa, cannabis dependence, cocaine dependence, conduct disorder, cyclothymic disorder, delirium,
 delusional disorder, dementia, dependent personality disorder, depression, dysthymic disorder,
 5 hallucinogen dependence, histrionic personality disorder, inhalant dependence, manic depression,
 multi-infarct dementia, narcissistic personality disorder, nicotine dependence, obsessive-compulsive
 disorder, opioid dependence, oppositional defiant disorder, panic disorder, paranoid personality disorder,
 phencyclidine dependence, phobia, posttraumatic stress disorder, schizoaffective disorder, schizoid
 personality disorder, schizophrenia, sedative dependence, separation anxiety disorder, and sleep
 10 disorder; a metabolic disorder such as Addison's disease, cerebrotendinous xanthomatosis, congenital
 adrenal hyperplasia, coumarin resistance, cystic fibrosis, fatty hepatocirrhosis,
 fructose-1,6-diphosphatase deficiency, galactosemia, goiter, glucagonoma, glycogen storage diseases,
 hereditary fructose intolerance, hyperadrenalism, hypoadrenalism, hyperparathyroidism,
 hypoparathyroidism, hypercholesterolemia, hyperthyroidism, hypoglycemia, hypothyroidism,
 15 hyperlipidemia, hyperlipemia, lipid myopathies, lipodystrophies, lysosomal storage diseases,
 mannosidosis, neuraminidase deficiency, obesity, osteoporosis, phenylketonuria, pseudovitamin D-
 deficiency rickets, disorders of carbohydrate metabolism such as congenital type II dyserythropoietic
 anemia, diabetes, insulin-dependent diabetes mellitus, non-insulin-dependent diabetes mellitus,
 galactose epimerase deficiency, glycogen storage diseases, lysosomal storage diseases, fructosuria,
 20 pentosuria, and inherited abnormalities of pyruvate metabolism, disorders of lipid metabolism such as
 fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase
 deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such
 Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy,
 adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier
 25 disease, hyperlipoproteinemia, lipodystrophy, lipomatoses, acute panniculitis, disseminated fat necrosis,
 adiposis dolorosa, lipid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis,
 hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary
 hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol
 acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-
 30 Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, and lipid myopathies, and disorders of
 copper metabolism such as Menke's disease, Wilson's disease, and Ehlers-Danlos syndrome type IX
 diabetes; and an endocrine disorder such as a disorder of the hypothalamus and/or pituitary resulting

from lesions such as a primary brain tumor, adenoma, infarction associated with pregnancy, hypophysectomy, aneurysm, vascular malformation, thrombosis, infection, immunological disorder, and complication due to head trauma, a disorder associated with hypopituitarism including hypogonadism, Sheehan syndrome, diabetes insipidus, Kallman's disease, Hand-Schuller-Christian disease, Letterer-Siwe disease, sarcoidosis, empty sella syndrome, and dwarfism, a disorder associated with hyperpituitarism including acromegaly, gigantism, and syndrome of inappropriate antidiuretic hormone (ADH) secretion (SIADH) often caused by benign adenoma, a disorder associated with hypothyroidism including goiter, myxedema, acute thyroiditis associated with bacterial infection, subacute thyroiditis associated with viral infection, autoimmune thyroiditis (Hashimoto's disease), and cretinism, a disorder associated with hyperthyroidism including thyrotoxicosis and its various forms, Grave's disease, pretibial myxedema, toxic multinodular goiter, thyroid carcinoma, and Plummer's disease, a disorder associated with hyperparathyroidism including Conn disease (chronic hypercalcemia), a pancreatic disorder such as Type I or Type II diabetes mellitus and associated complications, a disorder associated with the adrenals such as hyperplasia, carcinoma, or adenoma of the adrenal cortex, hypertension associated with alkalosis, amyloidosis, hypokalemia, Cushing's disease, Liddle's syndrome, and Arnold-Healy-Gordon syndrome, pheochromocytoma tumors, and Addison's disease, a disorder associated with gonadal steroid hormones such as: in women, abnormal prolactin production, infertility, endometriosis, perturbation of the menstrual cycle, polycystic ovarian disease, hyperprolactinemia, isolated gonadotropin deficiency, amenorrhea, galactorrhea, hermaphroditism, hirsutism and virilization, breast cancer, and, in post-menopausal women, osteoporosis, and, in men, Leydig cell deficiency, male climacteric phase, and germinal cell aplasia, a hypergonadal disorder associated with Leydig cell tumors, androgen resistance associated with absence of androgen receptors, syndrome of 5 α -reductase, and gynecomastia. Polynucleotides encoding NTRAN may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered NTRAN expression. Such qualitative or quantitative methods are well known in the art.

In a particular embodiment, polynucleotides encoding NTRAN may be used in assays that detect the presence of associated disorders, particularly those mentioned above. Polynucleotides complementary to sequences encoding NTRAN may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and

compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of polynucleotides encoding NTRAN in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical
5 trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of NTRAN, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding NTRAN, under conditions suitable for hybridization or
10 amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

15 Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

20 With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier, thereby preventing the development or further
25 progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding NTRAN may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced *in vitro*. Oligomers will preferably contain a fragment of a polynucleotide encoding NTRAN, or a fragment of a polynucleotide complementary to the polynucleotide encoding
30 NTRAN, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from polynucleotides encoding NTRAN may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from polynucleotides encoding NTRAN are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

SNPs may be used to study the genetic basis of human disease. For example, at least 16 common SNPs have been associated with non-insulin-dependent diabetes mellitus. SNPs are also useful for examining differences in disease outcomes in monogenic disorders, such as cystic fibrosis, sickle cell anemia, or chronic granulomatous disease. For example, variants in the mannose-binding lectin, MBL2, have been shown to be correlated with deleterious pulmonary outcomes in cystic fibrosis. SNPs also have utility in pharmacogenomics, the identification of genetic variants that influence a patient's response to a drug, such as life-threatening toxicity. For example, a variation in N-acetyl transferase is associated with a high incidence of peripheral neuropathy in response to the anti-tuberculosis drug isoniazid, while a variation in the core promoter of the ALOX5 gene results in diminished clinical response to treatment with an anti-asthma drug that targets the 5-lipoxygenase pathway. Analysis of the distribution of SNPs in different populations is useful for investigating genetic drift, mutation, recombination, and selection, as well as for tracing the origins of populations and their migrations (Taylor, J.G. et al. (2001) Trends Mol. Med. 7:507-512; Kwok, P.-Y. and Z. Gu (1999) Mol. Med. Today 5:538-543; Nowotny, P. et al. (2001) Curr. Opin. Neurobiol. 11:637-641).

Methods which may also be used to quantify the expression of NTRAN include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves (Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236). The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotides described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, NTRAN, fragments of NTRAN, or antibodies specific for NTRAN may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time (Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 5,840,484; hereby expressly incorporated by reference herein). Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression *in vivo*, as in the case of a tissue or biopsy sample, or *in vitro*, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention
5 may also be used in conjunction with *in vitro* model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) *Mol. Carcinog.* 24:153-159; Steiner, S. and N.L. Anderson (2000)
10 *Toxicol. Lett.* 112-113:467-471). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as
15 well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity (see, for example, Press Release 00-02
20 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>). Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In an embodiment, the toxicity of a test compound can be assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the
25 treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

30 Another embodiment relates to the use of the polypeptides disclosed herein to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually

to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of interest. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for NTRAN to quantify the levels of NTRAN expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoz, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art (Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662). Various types of microarrays are well known and thoroughly described in Schena, M., ed. (1999; DNA Microarrays: A Practical Approach, Oxford University Press, London).

In another embodiment of the invention, nucleic acid sequences encoding NTRAN may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries (Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; Trask, B.J. (1991) Trends Genet. 7:149-154). Once mapped, the nucleic acid sequences may be used to develop genetic linkage maps, for example, which

correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP) (Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357).

Fluorescent *in situ* hybridization (FISH) may be correlated with other physical and genetic map data (Heinz-Ulrich, et al. (1995) in Meyers, *supra*, pp. 965-968). Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding NTRAN on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

10 *In situ* hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely
15 localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (Gatti, R.A. et al. (1988) Nature 336:577-580). The nucleotide sequence of the instant invention may, also be used to detect differences in the chromosomal location due to translocation, inversion, etc.,
20 among normal, carrier, or affected individuals.

In another embodiment of the invention, NTRAN, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes
25 between NTRAN and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest (Geysen, et al. (1984) PCT application WO84/03564). In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with NTRAN, or fragments thereof, and washed.
30 Bound NTRAN is then detected by methods well known in the art. Purified NTRAN can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding NTRAN specifically compete with a test compound for binding NTRAN. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with NTRAN.

5 In additional embodiments, the nucleotide sequences which encode NTRAN may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding
10 description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/340,798, U.S. Ser. No. 60/365,645, U.S. Ser. No. 60/367,662, U.S. Ser.
15 No. 60/379,887, and U.S. Ser. No. 60/384,639, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD
20 database (Incyte Genomics, Palo Alto CA). Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Invitrogen), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and
25 ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively,
30 RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA

libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Invitrogen), using the recommended procedures or similar methods known in the art (Ausubel et al., *supra*, ch. 5). Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were
5 ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Biosciences) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUEScript plasmid
10 (Stratagene), PSPORT1 plasmid (Invitrogen, Carlsbad CA), PCDNA2.1 plasmid (Invitrogen), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B
15 from Invitrogen.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an
20 AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a
25 high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

30 III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such

as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Biosciences or supplied in ABI sequencing kits such as the

5 ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Amersham Biosciences); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art.

10 Reading frames within the cDNA sequences were identified using standard methods (Ausubel et al., *supra*, ch. 7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and

15 programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM; PROTEOME databases with sequences from *Homo sapiens*, *Rattus norvegicus*, *Mus musculus*, *Caenorhabditis elegans*, *Saccharomyces cerevisiae*,

20 *Schizosaccharomyces pombe*, and *Candida albicans* (Incyte Genomics, Palo Alto CA); hidden Markov model (HMM)-based protein family databases such as PFAM, INCY, and TIGRFAM (Haft, D.H. et al. (2001) *Nucleic Acids Res.* 29:41-43); and HMM-based protein domain databases such as SMART (Schultz, J. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:5857-5864; Letunic, I. et al. (2002) *Nucleic Acids Res.* 30:242-244). (HMM is a probabilistic approach which analyzes consensus

25 primary structures of gene families; see, for example, Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend

30 Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated

to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, the PROTEOME databases, BLOCKS, PRINTS, DOMO, 5 PRODOM, Prosite, hidden Markov model (HMM)-based protein family databases such as PFAM, INCY, and TIGRFAM; and HMM-based protein domain databases such as SMART. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (MiraiBio, Alameda CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the 10 MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second 15 column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

20 The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:23-44. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 2.

IV. Identification and Editing of Coding Sequences from Genomic DNA

25 Putative neurotransmission-associated proteins were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94; Burge, C. and S. Karlin (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to 30 form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan

predicted cDNA sequences encode neurotransmission-associated proteins, the encoded polypeptides were analyzed by querying against PFAM models for neurotransmission-associated proteins.

Potential neurotransmission-associated proteins were also identified by homology to Incyte cDNA sequences that had been annotated as neurotransmission-associated proteins. These selected

- 5 Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbprl public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription.
- 10 When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

15 **V. Assembly of Genomic Sequence Data with cDNA Sequence Data**

“Stitched” Sequences

- Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan
- 20 exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to
- 25 be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then “stitched” together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants.
- 30 Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared

by BLAST analysis to the genpept and gbprl public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

“Stretched” Sequences

5 Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in
10 Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were
15 therefore “stretched” or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of NTRAN Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:23-44 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other
20 implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:23-44 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Génethon were used to determine if any of the clustered sequences
25 had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between
30 chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid

markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

5 Association of a disease with a chromosomal locus can be determined by lod score. Lod score is a statistical method used to test the linkage of two or more loci within families having a genetic disease. The lod score is the logarithm to base 10 of the odds in favor of linkage. Linkage is defined as the tendency of two genes located on the same chromosome to be inherited together through meiosis (*Genetics in Medicine*, Fifth Edition, (1991) Thompson, M.W. et al., W.B. Saunders
10 Co. Philadelphia). A lod score of +3 or greater (1000:1 odds in favor of linkage) indicates a probability of 1 in 1000 that a particular marker was found solely by chance in affected individuals, which is strong evidence that two genetic loci are linked.

One such gene implicated in PD is PARK3, which maps to 2p13 (Gasser, T. et al. (1998) *Nature Genet.* 18:262-265). A marker at chromosomal position D2S441 was found to have a lod
15 score of 3.2 in the region of PARK3. This marker supported the disease association of PARK3 in the chromosomal interval from D2S134 to D2S286 (Gasser et al., *supra*). Markers located within chromosomal intervals D2S134 and D2S286, which map between 83.88 to 94.05 centiMorgans on the short arm of chromosome 2, were used to identify genes that map in the region between D2S134 and D2S286.

20 A second PD gene, implicated in early-onset recessive parkinsonism, is PARK6, located on chromosome 1 at 1p35-1p36. Several markers were obtained with lod scores greater than 3 including D1S199, D1S2732, D1S2828, D1S478, D1S2702, D1S2734, D1S2674 (Valente, E.M. et al, *supra*). These markers were used to determine the PD-relevant range of chromosome loci and identify sequences that map to chromosome 1 between D1S199 and D1S2885.

25 Restriction fragment length polymorphism (RFLP) markers shown to be near regions of DNA known as sequence-tagged sites (STS), have been mapped to NT_Contigs generated by the Human Genome Project using ePCR (Schuler, G.D. (1997) *Genome Research* 7: 541-550, and (1998) *Trends Biotechnol.* 16(11):456-9). Contigs containing regions of DNA with known disease-associated markers are therefore used to identify NTRAN sequences that map to disease-associated regions of
30 the genome.

Polynucleotides encoding NTRAN were mapped to NT_Contigs. Contigs longer than 1Mb were broken into subcontigs of 1Mb length with overlapping sections of 100kb. A preliminary step used

an algorithm, similar to MEGABLAST, to define the mRNA sequence /masked genomic DNA contig pairings. The cDNA/genomic pairings identified by the first algorithm were confirmed, and the NTRAN polynucleotides mapped to DNA contigs, using SIM4 (Florea, L. et al. (1998) Genome Res. 8:967-74, version May 2000) which had been optimized for high throughput processing and strand assignment confidence). The SIM4 output of the mRNA sequence/genomic contig pairs was further processed to determine the correct location of the NTRAN polynucleotides on the genomic contig, as well as their strand identity.

SEQ ID NO:40 was mapped to NT_Contig GBI:NT_005428_001.7 from Genbank release February 2002, covering a 9.65 Mb region of the genome that also contains PD-associated genetic markers D2S134 and D2S286. The maximum distance between SEQ ID NO:40 and markers D2S134 and D2S286, therefore, is 9.65 Mb. Thus, SEQ ID NO:40 is in proximity with genetic markers shown to consistently associate with PD.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound (Sambrook and Russell, *supra*, ch. 7; Ausubel et al., *supra*, ch. 4).

Analogous computer techniques applying BLAST were used to search for identical or related molecules in databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a

BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79%
5 identity and 100% overlap.

Alternatively, polynucleotides encoding NTRAN are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into
10 one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across
15 all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding NTRAN. cDNA sequences and cDNA library/tissue information are
20 found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of NTRAN Encoding Polynucleotides

Full length polynucleotides are produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to
25 initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

30 Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR

was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Biosciences), ELONGASE enzyme (Invitrogen), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

10 The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the
15 concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviII cholera virus endonuclease (Molecular Biology Research, Madison WI), and
20 sonicated or sheared prior to religation into pUC 18 vector (Amersham Biosciences). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Biosciences), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and
25 transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Biosciences) and Pfu DNA polymerase (Stratagene) with the following parameters: Step
30 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries

were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Biosciences) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

- 5 In like manner, full length polynucleotides are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Identification of Single Nucleotide Polymorphisms in NTRAN Encoding Polynucleotides

- 10 Common DNA sequence variants known as single nucleotide polymorphisms (SNPs) were identified in SEQ ID NO:23-44 using the LIFESEQ database (Incyte Genomics). Sequences from the same gene were clustered together and assembled as described in Example III, allowing the identification of all sequence variants in the gene. An algorithm consisting of a series of filters was used to distinguish SNPs from other sequence variants. Preliminary filters removed the majority of
15 basecall errors by requiring a minimum Phred quality score of 15, and removed sequence alignment errors and errors resulting from improper trimming of vector sequences, chimeras, and splice variants. An automated procedure of advanced chromosome analysis analysed the original chromatogram files in the vicinity of the putative SNP. Clone error filters used statistically generated algorithms to identify errors introduced during laboratory processing, such as those caused by reverse transcriptase,
20 polymerase, or somatic mutation. Clustering error filters used statistically generated algorithms to identify errors resulting from clustering of close homologs or pseudogenes, or due to contamination by non-human sequences. A final set of filters removed duplicates and SNPs found in immunoglobulins or T-cell receptors.

- Certain SNPs were selected for further characterization by mass spectrometry using the high
25 throughput MASSARRAY system (Sequenom, Inc.) to analyze allele frequencies at the SNP sites in four different human populations. The Caucasian population comprised 92 individuals (46 male, 46 female), including 83 from Utah, four French, three Venezualan, and two Amish individuals. The African population comprised 194 individuals (97 male, 97 female), all African Americans. The Hispanic population comprised 324 individuals (162 male, 162 female), all Mexican Hispanic. The
30 Asian population comprised 126 individuals (64 male, 62 female) with a reported parental breakdown of 43% Chinese, 31% Japanese, 13% Korean, 5% Vietnamese, and 8% other Asian. Allele frequencies were first analyzed in the Caucasian population; in some cases those SNPs which showed

no allelic variance in this population were not further tested in the other three populations.

X. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:23-44 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Biosciences), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25
5
10
superfine size exclusion dextran bead column (Amersham Biosciences). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon
15
membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

20 XI. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing; see, e.g., Baldeschweiler et al., *supra*), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Schena, M., ed.
25
(1999) DNA Microarrays: A Practical Approach, Oxford University Press, London). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and
30
may contain any appropriate number of elements (Schena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31).

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Biosciences). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte Genomics). Specific control poly(A)⁺ RNAs are synthesized by *in vitro* transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (Clontech, Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Biosciences).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and
5 coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in U.S. Patent No. 5,807,522, incorporated herein by reference. 1 μ l of the array element DNA, at an average concentration of 100 ng/ μ l, is loaded into the open capillary printing element by a high-speed robotic
10 apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2%
15 SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μ l of sample mixture consisting of 0.2 μ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with
20 an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μ l of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide
30 containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The
5 emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on
10 the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and
15 adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a
20 linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated
25 to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte Genomics). Array elements that exhibit at least about a two-fold change in expression, a signal-to-background ratio of at least about 2.5, and an element spot size of at least about 40%, are considered to be differentially expressed.

30 Expression

For example, SEQ ID NO:24 showed differential expression in lung squamous carcinoma tissues versus normal lung tissues as determined by microarray analysis. The expression of SEQ ID

NO:24 was decreased by at least two fold in lung squamous carcinoma tissues relative to grossly uninvolved normal lung tissue from the same donors. Therefore, SEQ ID NO:24 is useful as a diagnostic marker or as a potential therapeutic target for lung cancer.

5 SEQ ID NO:24 also showed differential expression in ovarian adenocarcinoma tissues versus normal ovarian tissues as determined by microarray analysis. The expression of SEQ ID NO:24 was decreased by at least two fold in ovarian adenocarcinoma tissues relative to grossly uninvolved normal ovarian tissue from the same donor. Therefore, SEQ ID NO:24 is useful as a diagnostic marker or as a potential therapeutic target for ovarian cancer.

10 Furthermore, SEQ ID NO:24 showed region-specific gene expression in the human brain as determined by microarray analysis. The expression of SEQ ID NO:24 was decreased by at least two fold in the cervical spinal cord relative to pooled brain tissues which were constituted from the major regions of the brain from two male brains; a 47 year old and a 48 year old. The tissue from the cervical spinal cord was isolated from a 47 year old male, the same 47 year old donor as in the pooled sample. Therefore, SEQ ID NO:24 serves as a useful biomarker for human brains, specifically for the
15 cervical spinal cord.

In an alternative example, the expression of SEQ ID NO:25, as determined by microarray analysis, was increased by at least two fold in sigmoid colon tissues relative to normal sigmoid colon tissues. The sigmoid colon tumor tissue which originated from a metastatic gastric sarcoma (stromal tumor) was harvested from a 48 year old female donor. The normal sigmoid colon tissue was
20 harvested from grossly uninvolved sigmoid colon tissue of the same donor. Therefore, SEQ ID NO:25 is useful as a diagnostic marker or as a potential therapeutic target for colon cancer.

SEQ ID NO:25 also showed decreased expression in tissue affected by lung adenocarcinoma versus normal lung tissue as determined by microarray analysis. A sample of right lung tissue that showed moderately differentiated adenocarcinoma was compared to grossly uninvolved lung tissue
25 from the same donor (Huntsman Cancer Institute, Salt Lake City, UT). Therefore, SEQ ID NO:25 is useful in diagnostic assays for and monitoring treatment of lung cancer.

Furthermore, the expression of SEQ ID NO:25, as determined by microarray analysis, was increased by at least two fold in Tangier disease-derived fibroblasts relative to normal fibroblasts. Both types of cells were cultured in the presence of cholesterol and compared with the same cell type
30 in the absence of cholesterol. The human fibroblasts were obtained from skin transplants from both normal subjects and two patients with homozygous Tangier disease. Cell lines were immortalized by transfection with human papillomavirus 16 genes E6 and E7 and a neomycin resistance selectable

marker. TD derived cells are deficient in an assay of apoA-I mediated tritiated cholesterol efflux. Therefore, SEQ ID NO:25 is useful in diagnostic assays for and monitoring treatment of Tangier disease.

In an alternative example, SEQ ID NO:30 showed decreased expression in lung tissue affected by squamous cell adenocarcinoma versus normal lung tissue as determined by microarray analysis. Grossly uninvolved lung tissue with no visible abnormalities, from a 73 year-old male, was compared to lung squamous cell adenocarcinoma tissue from the same donor (Roy Castle International Centre for Lung Cancer Research, Liverpool, UK). Therefore, SEQ ID NO:30 is useful in monitoring treatment of, and diagnostic assays for, lung cancer and other cell proliferative disorders.

As another example, SEQ ID NO:30 showed decreased expression in tissue affected by ovarian tumor versus normal ovary tissue as determined by microarray analysis. A normal ovary from a 79 year-old female donor was compared to an ovarian tumor from the same donor (Huntsman Cancer Institute, Salt Lake City, UT). Therefore, SEQ ID NO:30 is useful in monitoring treatment of, and diagnostic assays for, ovarian cancer and other cell proliferative disorders.

In an alternative example, SEQ ID NO:36 showed decreased expression in colon adenocarcinoma tissue versus grossly uninvolved colon tissue. Gene expression profiles were obtained by comparing normal colon tissue to colon tumor tissue from the same donor. Therefore, SEQ ID NO:36 is useful in monitoring treatment of, and diagnostic assays for, colon cancer and other cell proliferative disorders.

In an alternative example, SEQ ID NO:38 showed differential expression, as determined by microarray analysis. Array elements that exhibited about at least a two-fold change in expression and a signal intensity over 250 units, a signal-to-background ratio of at least 2.5, and an element spot size of at least 40% were identified as differentially expressed using the GEMTOOLS program (Incyte Genomics).

For example, the expression of cDNA from grossly uninvolved lung tissue from a 66 year-old male was compared to lung squamous cell carcinoma tissue from the same donor (Roy Castle International Centre for Lung Cancer Research, Liverpool, UK). The expression of SEQ ID NO:38 showed at least a two-fold increase in expression in the lung tumor tissue when compared to normal lung tissue expression levels from the same donor. Thus, SEQ ID NO:38 is useful for monitoring progression of, and diagnostic assays for, lung cancers.

In another example, specific dissected brain regions from a normal 61-year-old female were compared to dissected regions from the brain of a 79-year-old-female with severe Alzheimer's

disease (AD). The diagnosis of normal or severe AD was established by a certified neuropathologist based on microscopic examination of multiple sections throughout the brain. The expression of SEQ ID NO:38 showed at least a two-fold decrease in expression in the amygdala and anterior hippocampus brain regions when compared to the same brain regions from the normal 61-year-old female. Therefore, SEQ ID NO:38 is also useful for monitoring progression of, and diagnostic assays for, Alzheimer's disease.

In another example, SEQ ID NO:41 showed tissue-specific expression. RNA samples isolated from a variety of normal human tissues were compared to a common reference sample. Tissues contributing to the reference sample were selected for their ability to provide a complete distribution of RNA in the human body and include brain (4%), heart (7%), kidney (3%), lung (8%), placenta (46%), small intestine (9%), spleen (3%), stomach (6%), testis (9%), and uterus (5%). The normal tissues assayed were obtained from at least three different donors. RNA from each donor was separately isolated and individually hybridized to the microarray. Since these hybridization experiments were conducted using a common reference sample, differential expression values are directly comparable from one tissue to another. The expression of SEQ ID NO:41 was increased by at least two-fold in brain (amygdaloid body, occipital cortex, and parietal cortex) tissues as compared to the reference sample. Therefore, SEQ ID NO:41 can be used as a marker for brain tissues.

XII. Complementary Polynucleotides

Sequences complementary to the NTRAN-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring NTRAN. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of NTRAN. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the NTRAN-encoding transcript.

XIII. Expression of NTRAN

Expression and purification of NTRAN is achieved using bacterial or virus-based expression systems. For expression of NTRAN in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory

element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express NTRAN upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of NTRAN in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant *Autographica californica* nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding NTRAN by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect *Spodoptera frugiperda* (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus (Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945).

In most expression systems, NTRAN is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from *Schistosoma japonicum*, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Biosciences). Following purification, the GST moiety can be proteolytically cleaved from NTRAN at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel et al. (*supra*, ch. 10 and 16). Purified NTRAN obtained by these methods can be used directly in the assays shown in Examples XVII and XVIII, where applicable.

25 XIV. Functional Assays

NTRAN function is assessed by expressing the sequences encoding NTRAN at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT plasmid (Invitrogen, Carlsbad CA) and PCR3.1 plasmid (Invitrogen), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional

plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994; Flow Cytometry, Oxford, New York NY).

The influence of NTRAN on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding NTRAN and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding NTRAN and other genes of interest can be analyzed by northern analysis or microarray techniques.

XV. Production of NTRAN Specific Antibodies

NTRAN substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize animals (e.g., rabbits, mice, etc.) and to produce antibodies using standard protocols.

Alternatively, the NTRAN amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art (Ausubel et al., *supra*, ch. 11).

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity (Ausubel et al., *supra*). Rabbits are immunized with the oligopeptide-KLH
5 complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-NTRAN activity by, for example, binding the peptide or NTRAN to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XVI. Purification of Naturally Occurring NTRAN Using Specific Antibodies

Naturally occurring or recombinant NTRAN is substantially purified by immunoaffinity
10 chromatography using antibodies specific for NTRAN. An immunoaffinity column is constructed by covalently coupling anti-NTRAN antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Biosciences). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing NTRAN are passed over the immunoaffinity column, and the column is
15 washed under conditions that allow the preferential absorbance of NTRAN (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/NTRAN binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and NTRAN is collected.

XVII. Identification of Molecules Which Interact with NTRAN

20 NTRAN, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent (Bolton, A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539). Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled NTRAN, washed, and any wells with labeled NTRAN complex are assayed. Data obtained using different concentrations of NTRAN are used to calculate values for the number, affinity, and association of NTRAN with the
25 candidate molecules.

Alternatively, molecules interacting with NTRAN are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989; *Nature* 340:245-246), or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

NTRAN may also be used in the PATHCALLING process (CuraGen Corp., New Haven
30 CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVIII. Demonstration of NTRAN Activity

An assay for NTRAN activity measures the expression of NTRAN on the cell surface. cDNA encoding NTRAN is transfected into an appropriate mammalian cell line. Cell surface proteins are labeled with biotin as described (de la Fuente, M.A. et al. (1997) Blood 90:2398-2405).

- 5 Immunoprecipitations are performed using NTRAN-specific antibodies, and immunoprecipitated samples are analyzed using sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and immunoblotting techniques. The ratio of labeled immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of NTRAN expressed on the cell surface.

- In the alternative, an assay for NTRAN activity is based on a prototypical assay for
 10 ligand/receptor-mediated modulation of cell proliferation. This assay measures the rate of DNA synthesis in Swiss mouse 3T3 cells. A plasmid containing polynucleotides encoding NTRAN is added to quiescent 3T3 cultured cells using transfection methods well known in the art. The transiently transfected cells are then incubated in the presence of [³H]thymidine, a radioactive DNA precursor molecule. Varying amounts of NTRAN ligand are then added to the cultured cells. Incorporation of
 15 [³H]thymidine into acid-precipitable DNA is measured over an appropriate time interval using a radioisotope counter, and the amount incorporated is directly proportional to the amount of newly synthesized DNA. A linear dose-response curve over at least a hundred-fold NTRAN ligand concentration range is indicative of receptor activity. One unit of activity per milliliter is defined as the concentration of NTRAN producing a 50% response level, where 100% represents maximal
 20 incorporation of [³H]thymidine into acid-precipitable DNA (McKay, I. and I. Leigh, eds. (1993) Growth Factors: A Practical Approach, Oxford University Press, New York NY, p. 73.)

- In a further alternative, the assay for NTRAN activity is based upon the ability of GPCR family proteins to modulate G protein-activated second messenger signal transduction pathways (e.g., cAMP; Gaudin, P. et al. (1998) J. Biol. Chem. 273:4990-4996). A plasmid encoding full length
 25 NTRAN is transfected into a mammalian cell line (e.g., Chinese hamster ovary (CHO) or human embryonic kidney (HEK-293) cell lines) using methods well-known in the art. Transfected cells are grown in 12-well trays in culture medium for 48 hours, then the culture medium is discarded, and the attached cells are gently washed with PBS. The cells are then incubated in culture medium with or without ligand for 30 minutes, then the medium is removed and cells lysed by treatment with 1 M
 30 perchloric acid. The cAMP levels in the lysate are measured by radioimmunoassay using methods well-known in the art. Changes in the levels of cAMP in the lysate from cells exposed to ligand compared to those without ligand are proportional to the amount of NTRAN present in the transfected

cells.

To measure changes in inositol phosphate levels, the cells are grown in 24-well plates containing 1×10^5 cells/well and incubated with inositol-free media and [^3H]myoinositol, 2 mCi/well, for 48 hr. The culture medium is removed, and the cells washed with buffer containing 10 mM LiCl followed by addition of ligand. The reaction is stopped by addition of perchloric acid. Inositol phosphates are extracted and separated on Dowex AG1-X8 (Bio-Rad) anion exchange resin, and the total labeled inositol phosphates counted by liquid scintillation. Changes in the levels of labeled inositol phosphate from cells exposed to ligand compared to those without ligand are proportional to the amount of NTRAN present in the transfected cells.

In a further alternative, the ion conductance capacity of NTRAN is demonstrated using an electrophysiological assay. NTRAN is expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector encoding NTRAN. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A small amount of a second plasmid, which expresses any one of a number of marker genes such as β -galactosidase, is co-transformed into the cells in order to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of NTRAN and β -galactosidase. Transformed cells expressing β -galactosidase are stained blue when a suitable colorimetric substrate is added to the culture media under conditions that are well known in the art. Stained cells are tested for differences in membrane conductance due to various ions by electrophysiological techniques that are well known in the art. Untransformed cells, and/or cells transformed with either vector sequences alone or β -galactosidase sequences alone, are used as controls and tested in parallel. The contribution of NTRAN to cation or anion conductance can be shown by incubating the cells using antibodies specific for either NTRAN. The respective antibodies will bind to the extracellular side of NTRAN, thereby blocking the pore in the ion channel, and the associated conductance. To study the dependence of NAP on external ions, sodium can be replaced by choline or N-methyl-D-glucamine and chloride by gluconate, NO_3 , or SO_4 (Kavanaugh, M.P. et al. (1992) J. Biol. Chem. 267:22007-22009).

In a further alternative, NTRAN transport activity is assayed by measuring uptake of labeled substrates into *Xenopus laevis* oocytes. Oocytes at stages V and VI are injected with NTRAN mRNA (10 ng per oocyte) and incubated for 3 days at 18°C in OR2 medium (82.5 mM NaCl, 2.5 mM KCl, 1 mM CaCl_2 , 1 mM MgCl_2 , 1 mM Na_2HPO_4 , 5 mM Hepes, 3.8 mM NaOH, 50 $\mu\text{g/ml}$

gentamycin, pH 7.8) to allow expression of NTRAN protein. Oocytes are then transferred to standard uptake medium (100 mM NaCl, 2 mM KCl, 1 mM CaCl₂, 1 mM MgCl₂, 10 mM Hepes/Tris pH 7.5). Uptake of various substrates (e.g., amino acids, sugars, drugs, and neurotransmitters) is initiated by adding a ³H substrate to the oocytes. After incubating for 30 minutes, uptake is terminated
5 by washing the oocytes three times in Na⁺-free medium, measuring the incorporated ³H, and comparing with controls. NTRAN activity is proportional to the level of internalized ³H substrate.

In a further alternative, NTRAN activity can be demonstrated using an electrophysiological assay for ion conductance. Capped NTRAN mRNA transcribed with T7 polymerase is injected into defolliculated stage V *Xenopus* oocytes, similar to the previously described method. Two to seven
10 days later, transport is measured by two-electrode voltage clamp recording. Two-electrode voltage clamp recordings are performed at a holding potential of 50 mV. The data are filtered at 10 Hz and recorded with the MacLab digital-to-analog converter and software for data acquisition and analysis (AD Instruments, Castle Hill, Australia). To study the dependence of NTRAN on external ions, sodium can be replaced by choline or N-methyl-D-glucamine and chloride by gluconate, NO₃, or SO₄
15 (Kavanaugh, M.P. et al. (1992) J. Biol. Chem. 267:22007-22009).

Calmodulin-binding activity of NTRAN can be demonstrated by mixing 1.5 ml of 0.2 μM calmodulin with increasing concentrations of NTRAN (30 μl in concentrations ranging from 0.5 to 3.1 μM). Analysis of binding activity is determined by Scatchard representation. The bound NTRAN is calculated as $\Delta N / \Delta N_{\max 200} \times [\text{total calmodulin}]$. The free NTRAN concentration is calculated as [total
20 NTRAN] - [bound NTRAN]. (Bosc, C. et al. (2001) J. Biol. Chem. 276:30904-30913).

Alternatively, calmodulin-binding activity of NTRAN can be determined in a binding assay using calmodulin Sepharose beads. Calmodulin Sepharose 6B beads (1 mg/ml calmodulin) are equilibrated in 20 mM Hepes-KOH, pH 7.2, 0.15 M NaCl, 5 mg/ml bovine serum albumin, 0.02% Triton X-100 (v/v) (buffer C) and either 2.5 mM CaCl₂ or 5 mM EGTA. Samples of NTRAN are
25 incubated with 5 μl of calmodulin-Sepharose 6B beads for 3 hours at 22°C in 0.5 ml of buffer C in the presence or absence (5 mM EGTA) of 2.5 mM CaCl₂. Subsequently, beads are pelleted by centrifugation at 1000 x g and washed five times (1.5 ml each wash) with modified buffer C (Triton X-100 concentration is increased to 0.1% (v/v) and albumin is omitted), by resuspension and centrifugation at 1000 x g. Washed beads containing bound ligand are incubated in 0.1 ml of SDS gel
30 loading buffer for 5 minutes at 95°C. Bound NTRAN is visualized by Western immunoblotting. (Rossi, E.A. et al. (1999) J. Biol. Chem. 274:27201-27210).

Sialic acid-binding activity of NTRAN can be demonstrated in a COS cell binding assay.

COS cells are transfected with plasmids encoding full-length NTRAN using DEAE-dextran as described in Simmons D.L. (1993) Cloning cell surface molecules by transient expression in mammalian cells. In Cellular Interactions in Development — A Practical Approach. Edited by Hartley D.A.. Oxford: IRL Press, 93–128. On the third day after transfection, binding assays with
5 erythrocytes are carried out for 1 hour at 37 °C in DMEM culture medium with 0.2 % BSA. Unbound erythrocytes are washed off and the cells are fixed in 0.25 % glutardialdehyde. To assess the effect of antibodies on binding, COS cells are pre-incubated with immunoglobulins at 20 µg/ml for 1 hour prior to the addition of erythrocytes (Kelm, S. et al. (1994) Curr. Biol. 4:965-972).

In the alternative, choline transporter activity or choline-transporter-like CTL1 protein activity
10 of NTRAN is determined by measuring choline uptake by yeast transformed with expression vectors harboring polynucleotides encoding NTRAN. The assay is performed in nitrogen-free medium at 30°C for 10 or 30 min in the presence of 25 nM [³H]choline. The cells are then filtered, and washed. The amount of [³H]choline present in the cells is proportional to the activity of NTRAN in the cells (O'Regan, S. *supra*).

15 In a further alternative, NTRAN protein kinase (PK) activity is measured by phosphorylation of a protein substrate using gamma-labeled [³²P]-ATP and quantitation of the incorporated radioactivity using a gamma radioisotope counter. NTRAN is incubated with the protein substrate, [³²P]-ATP, and an appropriate kinase buffer. The ³²P incorporated into the product is separated from free [³²P]-ATP by electrophoresis and the incorporated ³²P is counted. The amount of ³²P recovered
20 is proportional to the PK activity of NTRAN in the assay. A determination of the specific amino acid residue phosphorylated is made by phosphoamino acid analysis of the hydrolyzed protein.

An assay for NTRAN activity measures the expression of NTRAN on the cell surface. cDNA encoding NTRAN is transfected into a non-leukocytic cell line. Cell surface proteins are labeled with biotin (de la Fuente, M.A. et al. (1997) Blood 90:2398-2405). Immunoprecipitations are
25 performed using NTRAN-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of NTRAN expressed on the cell surface.

Alternatively, an assay for NTRAN activity measures the amount of cell aggregation induced by overexpression of NTRAN. In this assay, cultured cells such as NIH3T3 are transfected with
30 cDNA encoding NTRAN contained within a suitable mammalian expression vector under control of a strong promoter. Cotransfection with cDNA encoding a fluorescent marker protein, such as Green Fluorescent Protein (CLONTECH), is useful for identifying stable transfectants. The amount of cell

agglutination, or clumping, associated with transfected cells is compared with that associated with untransfected cells. The amount of cell agglutination is a direct measure of NTRAN activity.

Alternatively, an assay for NTRAN activity measures the disruption of cytoskeletal filament networks upon overexpression of NTRAN in cultured cell lines (Reznicek, G. A. et al. (1998) J. Cell Biol. 141:209-225). cDNA encoding NTRAN is subcloned into a mammalian expression vector that drives high levels of cDNA expression. This construct is transfected into cultured cells, such as rat kangaroo PtK2 or rat bladder carcinoma 804G cells. Actin filaments and intermediate filaments such as keratin and vimentin are visualized by immunofluorescence microscopy using antibodies and techniques well known in the art. The configuration and abundance of cytoskeletal filaments can be assessed and quantified using confocal imaging techniques. In particular, the bundling and collapse of cytoskeletal filament networks is indicative of NTRAN activity.

Alternatively, cell adhesion activity in NTRAN is measured in a 96-well plate in which wells are first coated with NTRAN by adding solutions of NTRAN of varying concentrations to the wells. Excess NTRAN is washed off with saline, and the wells incubated with a solution of 1% bovine serum albumin to block non-specific cell binding. Aliquots of a cell suspension of a suitable cell type are then added to the wells and incubated for a period of time at 37 °C. Non-adherent cells are washed off with saline and the cells stained with a suitable cell stain such as Coomassie blue. The intensity of staining is measured using a variable wavelength multi-well plate reader and compared to a standard curve to determine the number of cells adhering to the NTRAN coated plates. The degree of cell staining is proportional to the cell adhesion activity of NTRAN in the sample.

Various modifications and variations of the described compositions, methods, and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. It will be appreciated that the invention provides novel and useful proteins, and their encoding polynucleotides, which can be used in the drug discovery process, as well as methods for using these compositions for the detection, diagnosis, and treatment of diseases and conditions. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Nor should the description of such embodiments be considered exhaustive or limit the invention to the precise forms disclosed. Furthermore, elements from one embodiment can be readily recombined with elements from one or more other embodiments. Such combinations can form a number of embodiments within the scope of the invention. It is intended that the scope of the invention be

defined by the following claims and their equivalents.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Incyte Full Length Clones
7506758	1	7506758CD1	23	7506758CB1	
4381669	2	4381669CD1	24	4381669CB1	
7503554	3	7503554CD1	25	7503554CB1	5371744CA2
7506077	4	7506077CD1	26	7506077CB1	1977274CA2
7506765	5	7506765CD1	27	7506765CB1	90039685CA2
7490048	6	7490048CD1	28	7490048CB1	
2133585	7	2133585CD1	29	2133585CB1	2133585CA2
7509063	8	7509063CD1	30	7509063CB1	
5496710	9	5496710CD1	31	5496710CB1	
72150826	10	72150826CD1	32	72150826CB1	
6799476	11	6799476CD1	33	6799476CB1	
7509488	12	7509488CD1	34	7509488CB1	
7510060	13	7510060CD1	35	7510060CB1	90087674CA2
7510226	14	7510226CD1	36	7510226CB1	
7510385	15	7510385CD1	37	7510385CB1	
7511618	16	7511618CD1	38	7511618CB1	
6244135	17	6244135CD1	39	6244135CB1	5059410CA2
7506689	18	7506689CD1	40	7506689CB1	95116857CA2
7510185	19	7510185CD1	41	7510185CB1	90196537CA2
1420867	20	1420867CD1	42	1420867CB1	1420867CA2
7512289	21	7512289CD1	43	7512289CB1	
7512447	22	7512447CD1	44	7512447CB1	

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
1	7506758CD1	g13647037	2.3E-56	[Mus musculus] synaptotagmin-like protein 3-a (Fukuda, M. et al. (2001) Biochem. Biophys. Res. Commun. 283:513-519.)
		418460 Syt4	7.3E-27	[Mus musculus][Small molecule-binding protein] Synaptotagmin-like 4 (granuphiin), a rabphilin-3-like effector of rab family proteins involved in vesicle transport, binds phospholipids in a Ca(2+)-independent manner, may play a role in exocytosis of dense-core granules in endocrine tissues (Wang, J. et al. (1999) J. Biol. Chem. 274:28542-28548; Matesic, L. E. et al. (2001) Proc. Natl. Acad. Sci. U S A 98:10238-10243.)
		432508 RPH3AL	1.8E-11	[Homo sapiens][Cytoplasmic] Putative zinc finger protein with similarity to the N-terminal region of rabphilin-3A, may regulates exocytosis in endocrine cells, is a candidate gene located in 17p13.3 medulloblastoma tumor suppressor locus (Haynes, L. P. et al. (2001) J. Biol. Chem. 276:9726-9732.)
2	4381669CD1	g10880799	0.0	[Mus musculus] Syne-1B (Apel, E. D. et al. (2000) J. Biol. Chem. 275:31986-31995.)
		628322 Syne1	0.0	[Mus musculus][Nuclear] Synaptic nuclear envelope 1, contains multiple spectrin repeats and localizes to the nuclear envelope, enriched in synaptic nuclei at neuromuscular junctions, may function in nuclear migration or anchoring (Apel, E. D. et al. (2000) <u>supra</u> .)
		622033 SYNE-2	1.4E-276	[Homo sapiens][Structural protein][Cytoskeletal] Protein containing spectrin repeats, has similarity to mouse Syne1 and to Drosophila Klarsicht, which is associated with the nuclei of fly photoreceptor cells (Apel, E. D. et al. (2000) <u>supra</u> .)
3	7503554CD1	g13936383	4.7E-184	[Homo sapiens] neuronal leucine-rich repeat protein-3
		748481 FLJ1112 ₉	4.1E-185	[Homo sapiens] Protein containing leucine rich repeats, which mediate protein-protein interactions and a leucine rich repeat N-terminal cysteine rich domain (Fukamachi, K. et al. (2001) Biochem. Biophys. Res. Commun. 287:257-263.)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
3 cont		419907 Lrrn3	2.4E-173	[Mus musculus] Brain leucine rich repeat protein, a member of the leucine-rich repeat family of proteins involved in protein-protein interactions, possibly functions in nervous system development and maintenance (Taniguchi, H. et al. (1996) Brain Res. Mol. Brain Res. 36:45-52; Ishii, N. et al. (1996) Brain Res. Mol. Brain Res. 40:148-152.)
4	7506077CD1	g4102729 334702 CLN3	8.0E-182 7.0E-183	[Homo sapiens] CLN3 protein [Homo sapiens][Chaperones][Lysosome/vacuole; Cytoplasmic; Mitochondrial] Ceroid-lipofuscinosis neuronal 3, plays a role in lysosomal pH homeostasis; mutation of the corresponding gene is detected in patients with juvenile neuronal ceroid lipofuscinosis (Batten disease), a lysosomal storage disease (Golabek, A. A. et al. Mol. Genet. Metab. 70:203-213; Lehtovirta, M. et al. (2001) Hum. Mol. Genet. 10:69-75.)
		318588 Cln3	1.1E-151	[Mus musculus][Lysosome/vacuole; Golgi; Cytoplasmic; Mitochondrial] Ceroid-lipofuscinosis neuronal 3, targeted disruption produces mice with a neuronal storage disorder resembling that seen in Batten disease patients; mutation of human CLN3 is detected in patients with juvenile neuronal ceroid lipofuscinosis (Mitchison, H. M. et al. (1999) The Batten Mouse Model Consortium, Neurobiol. Dis. 6:321-334.)
5	7506765CD1	g14278927 429678 C1qrf	3.0E-86 2.5E-73	[Mus musculus] gliacolin [Mus musculus] C1q-related factor, has a collagenous region and a globular domain and has similarity to the C1q signature domain, highly expressed in brain areas that are involved in motor function (Berube, N. G. et al. (1999) Brain Res. Mol. Brain Res. 63:233-240.)
		567880 CRF	8.6E-73	[Homo sapiens] C1q-related factor, has a collagenous region and a globular domain and has similarity to the C1q signature domain, highly expressed in brain areas that are involved in motor function (Berube, N. G. et al. (1999) <i>supra</i> .)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
6	7490048CD1	g6601555	0.0	[Rattus norvegicus] glutamate receptor interacting protein 2 Dong, H., et al. (1999) J. Neurosci. 19:6930-6941 Characterization of the glutamate receptor-interacting proteins GRIP1 and GRIP2
		734373[Rn.15680	0.0	[Rattus norvegicus] [Anchor Protein] [Unspecified membrane] Glutamate receptor interacting protein 2, an adaptor protein that has two sets of three PDZ domains, may act as a scaffold protein that anchors AMPA glutamate receptors at excitatory synapses and is localized within lipid rafts of the plasma membrane
		425390[GRIP1	3.20E-237	[Homo sapiens] [Structural protein; DNA-binding protein; Transcription factor] [Nuclear; Plasma membrane] Glutamate receptor interacting protein, transcriptional coactivator involved in estrogen signaling, interacts specifically with ephrin B1 (EPHB1) to form heterodimers that make a scaffolding framework for multiprotein signaling complexes formation Shang, Y., et al. (2000) Cell 103:843-852 Cofactor dynamics and sufficiency in estrogen receptor-regulated transcription.
7	2133585CD1	g1685069	5.2E-226	[Homo sapiens] sushi-repeat-containing protein precursor Meindl, A. et al. (1995) Hum. Mol. Genet. 4:2339-2346 A gene (SRPX) encoding a sushi-repeat-containing protein is deleted in patients with X-linked retinitis pigmentosa.
		343818[SRPX	4.50E-227	[Homo sapiens] [Unspecified membrane] Sushi-repeat-containing protein (X chromosome), may be involved in negative regulation of cell growth, expression is reduced in several cancer cell lines; mutation of the corresponding gene may be associated with X-linked retinitis pigmentosa (XLRP) Shimakage, M. et al. (2000) Int. J. Cancer 87:5-11 Down-regulation of drs mRNA in human colon adenocarcinomas.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
7 cont		629524 Drs	7.40E-211	[Rattus norvegicus] [Plasma membrane] Sushi-repeat-containing protein (X chromosome), protein suppressed in v-src-transformed cells, may be involved in inhibition of transformation; mutation of the human SRPX may be associated with X-linked retinitis pigmentosa (XLRP)
8	7509063CD1	g10880799	0.0	[Mus musculus] Syne-1B Apel, E.D. (2000) J. Biol. Chem. 275:31986-31995 Syne-1, A Dystrophin- and Klarsicht-related Protein Associated with Synaptic Nuclei at the Neuromuscular Junction.
		628322 Syne1	0.0	[Mus musculus] [Nuclear] Synaptic nuclear envelope 1, contains multiple spectrin repeats and localizes to the nuclear envelope, enriched in synaptic nuclei at neuromuscular junctions, may function in nuclear migration or anchoring
		622033 SYNE-2	1.90E-268	[Homo sapiens] [Structural protein] [Cytoskeletal] Protein containing spectrin repeats, has similarity to mouse Syne1 and to Drosophila Klarsicht, which is associated with the nuclei of fly photoreceptor cells
9	5496710CD1	g18390059	0.0	cell recognition protein CASPR4 [Homo sapiens]
		g12330704	0.0	[Mus musculus] cell recognition molecule CASPR4
		336668 CNTNAP1	4.20E-255	[Homo sapiens] [Receptor (signalling)] [Unspecified membrane; Plasma membrane] Neurexin 4 (contactin associated protein 1), a neuronal paranodal transmembrane receptor containing epidermal growth factor-like and neurexin motifs, binds contactin (CNTN1), may have a role in neuronal intracellular signaling Peles, E. et al. (1997) EMBO J. 16:978-988 Identification of a novel contactin-associated transmembrane receptor with multiple domains implicated in protein-protein interactions.
		587769 Nrxn4	2.30E-252	[Mus musculus] [Receptor (signalling)] [Unspecified membrane; Plasma membrane] Neurexin 4 (contactin associated protein 1), a putative neuronal paranodal transmembrane receptor, may have a role in neuronal intracellular signaling; mutant animals display defects in axonogenesis

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
10	72150826CD1	g211123	2.9E-94	[Gallus gallus] agrin-related protein 1 Ruegg, M.A.(1992) Neuron 8:691-699 The agrin gene codes for a family of basal lamina proteins that differ in function and distribution.
		328066 Agrn	5.50E-90	[Rattus norvegicus] [Inhibitor or repressor] [Extracellular matrix (cuticle and basement membrane); Basement membrane (extracellular matrix); Extracellular (excluding cell wall)] Agrin, proteoglycan component of the basal lamina that stimulates acetylcholine receptor aggregation through the activation of MUSK, involved in synaptogenesis
		310445 AGRN	4.30E-89	[Homo sapiens] [Inhibitor or repressor] [Extracellular matrix (cuticle and basement membrane); Basement membrane (extracellular matrix); Extracellular (excluding cell wall)] Agrin, a component of the basement membrane, mediates acetylcholine receptor clustering, likely through the activation of MUSK, may promote amyloidogenic peptide aggregation in Alzheimer's disease Berzin, T. M. et al. (2000) Neurobiol. Aging 21:349-355 Agrin and microvascular damage in Alzheimer's disease.
11	6799476CD1	g11558246	0.0	[Mus musculus] calyntenin-1 protein Vogt, L., et al. (2001) Mol. Cell. Neurosci. 17:151-166 Calyntenin-1, a Proteolytically Processed Postsynaptic Membrane Protein with a Cytoplasmic Calcium-Binding Domain.
		570390 KIAA0911	0.0	[Homo sapiens] Protein containing cadherin domains, which are found in the extracellular domain of some receptors and cell adhesion proteins
		626171 CS2	6.50E-299	[Homo sapiens] Protein containing two cadherin domains, which are found in the extracellular domain of some receptors and cell adhesion proteins, has strong similarity to uncharacterized calyntenin-2 (mouse Cstm2)
12	7509488CD1	g11558246	0.0	[Mus musculus] calyntenin-1 protein Vogt, L., et al., supra

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
12 cont		570390 K1AA091 1	0	[Homo sapiens] Protein containing cadherin domains, which are found in the extracellular domain of some receptors and cell adhesion proteins
		626171 CS2	8.90E-302	[Homo sapiens] Protein containing two cadherin domains, which are found in the extracellular domain of some receptors and cell adhesion proteins, has strong similarity to uncharacterized calstn2n-2 (mouse Cstn2)
13	7510060CD1	g307156	0.0	[Homo sapiens] myelin-associated glycoprotein precursor Sato, S. et al. (1989) Biochem. Biophys. Res. Commun. 163:1473-1480 cDNA cloning and amino acid sequence for human myelin-associated glycoprotein.
		623760 MAG	0.0	[Homo sapiens][Plasma membrane] Myelin associated glycoprotein, a member of the sialoadhesin subgroup of immunoglobulin superfamily lectins which may play a role in cell adhesion; identified as an autoantigen in several forms of demyelinating neuropathy including multiple sclerosis Miescher, G. C. et al. (1997) Brain Res Mol Brain Res 52:299-306 Reciprocal expression of myelin-associated glycoprotein splice variants in the adult human peripheral and central nervous systems.
		591203 Mag	0.0	[Rattus norvegicus][Plasma membrane] Myelin-associated glycoprotein, a lectin which inhibits axon outgrowth and may play a role in cell adhesion; identified as an autoantigen in several forms of demyelinating neuropathy Royland, J. et al. (1992) Brain Res Dev Brain Res 65: 223-226 Down regulation of myelin-specific mRNAs in the mechanism of hypomyelination in the undernourished developing brain.
14	7510226CD1	g6851362	4.3E-93	[Homo sapiens] zinedin Castets, F. et al. (2000) J. Biol. Chem. 275, 19970-19977 Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat proteins principally expressed in the brain.

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
14 cont		432836 ZIN	3.5E-94	[Homo sapiens][Structural protein;Small molecule-binding protein][Cytoplasmic] Zinedin, contains WD-repeats and has similarity to the putative scaffolding protein striatin (STRN), binds calmodulin (CALM1) in a calcium sensitive-manner Castets, F. et al. <u>supra</u>
		609919 Strn	6.4E-45	[Rattus norvegicus][Small molecule-binding protein] Striatin, binds calmodulin in the presence of calcium, contains WD-repeats, possibly functions in excitatory synapse calcium-signaling pathways Castets, F. et al. (supra)
15	7510385CD1	g974284	7.3E-169	[Homo sapiens] semaphorin V Wei, M. H. et al. (1996) Cancer Res. 56, 1487-1492 Construction of a 600-kilobase cosmid clone contig and generation of a transcriptional map surrounding the lung cancer tumor suppressor gene (TSG) locus on human chromosome 3p21.3: progress toward the isolation of a lung cancer TSG
16	7511618CD1	g18254511	4.6E-185	[Homo sapiens] ubiquilin Mah, A. L. et al.
				Identification of ubiquilin, a novel presenilin interactor that increases presenilin protein accumulation J. Cell Biol. 151, 847-862 (2000)
		437284 UBQLN1	5.5E-185	[Homo sapiens][Endoplasmic reticulum;Nuclear;Cytoplasmic] Ubiquilin 1, a ubiquitin-related protein associated with the 26S proteasome, binds to and promotes the accumulation of PSEN1 and PSEN2, localizes to neurofibrillary tangles and Lewy bodies in brains affected by Alzheimer's disease and Parkinson's disease Kleijnen, M. F. et al.
				The hPLIC proteins may provide a link between the ubiquitination machinery and the proteasome. Mol Cell 6, 409-19 (2000).

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
16 cont		757282 Ubqln1	1.3E-160	[Rattus norvegicus] Protein with very strong similarity to ubiquitin 1 (mouse Ubqln1), which regulates the interaction between the plasma membrane and vimentin intermediate filaments, member of the ubiquitin family, contains two UBA (ubiquitin associated) or TS-N domains
17	6244135CD1	g200250	6.9E-40	Bedford, F. K. et al. Nat. Neurosci. 4, 908-916 (2001). [Mus musculus] PCD-5
				Nordquist, D. T. et al.
				cDNA cloning and characterization of three genes uniquely expressed in cerebellum by Purkinje neurons
				J. Neurosci. 8, 4780-4789 (1988)
		58237 Pcp2	5.6E-41	[Mus musculus] Purkinje cell protein 2, a novel guanyl nucleotide exchange factor that interacts with G protein Gnao, may have a role in retinal and central nervous system development, expression is confined to Purkinje cells within the cerebellum
				Sandhofer, C. et al.
				Beta receptor isoforms are not essential for thyroid hormone-dependent acceleration of PCP-2 and myelin basic protein gene expression in the developing brains of neonatal mice.
				Mol Cell Endocrinol 137, 109-15 (1998).
18	7506689CD1	g23468354	6.0E-65	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F [Homo sapiens]
		g4519503	3.0E-76	[Homo sapiens] semaphorin W
				Encinas, J. A. et al.
				Cloning, expression, and genetic mapping of Sema W, a member of the semaphorin family
				Proc. Natl. Acad. Sci. U.S.A. 96, 2491-2496 (1999)
		341226 SEMA4F	2.5E-77	[Homo sapiens][Plasma membrane] Semaphorin 4F (semaphorin W), a member of the semaphorin family, may be involved in neuronal growth cone guidance

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
18 cont				Encinas, J. A. et al. <u>supra</u>
		609873 Sema4f	1.7E-61	[Rattus norvegicus][Plasma membrane] Semaphorin 4F(semaphorin W), a member of the semaphorin family, involved in neuronal growth cone guidance, induces the collapse of growth cones
				Schulze, W. et al.
				Semaphorin4F interacts with the synapse-associated protein SAP90/PSD-95.
				J Neurochem 78, 482-9. (2001).
19	7510185CD1	g3068592	0.0	[Mus musculus] punc Salbaum, J. M. Mech. Dev. 71, 201-204 (1998) Salbaum, J. M. Mamm. Genome 10, 107-111 (1999)
		582679 Punc	0.0	[Mus musculus][Adhesin/agglutinin][Plasma membrane] Putative neuronal cell adhesion molecule, a member of the immunoglobulin superfamily of cell surface proteins, may play a role in cerebellar control of motor coordination and early embryogenesis Salbaum, J. M. Mech Dev 71, 201-4 (1998). Yang, W. et al. Mol Cell Biol 21, 6031-43 (2001).
		348156 PUNC	2.0E-162	[Homo sapiens][Adhesin/agglutinin][Plasma membrane] Putative neuronal cell adhesion molecule, a member of the immunoglobulin superfamily of cell surface proteins, highly expressed in the embryonic nervous system and limb buds Salbaum, J. M (1999, <u>supra</u>)
20	1420867CD1	g13235326	1.8E-89	[Homo sapiens] dJ47704.1.2 (novel protein similar to otoferlin and dysferlin, isoform 2)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
20 cont		341002 OTOF	1.3E-38	[Homo sapiens][Cytoplasmic; Unspecified membrane] Otoferlin, may play a role in synaptic or other vesicle membrane fusion and is required for inner ear function; alteration of the corresponding gene is associated with nonsyndromic prelingual deafness Yasunaga, S. et al. Nat Genet 21, 363-9 (1999). Yasunaga, S. et al. Am J Hum Genet 67, 591-600 (2000).
		710087 Otof	5.7E-38	[Mus musculus] Otoferlin, may play a role in synaptic or other vesicle membrane fusion; alteration of human OTOF is associated with nonsyndromic prelingual deafness Yasunaga, S. et al (1999, supra)
21	7512289CD1	g7658295	5.9E-122	[Homo sapiens] transmembrane protein BRI Vidal, R. et al. Proc. Natl. Acad. Sci. U.S.A. 97, 4920-4925 (2000)
		626041 ITM2B	1.8E-123	[Homo sapiens][Unspecified membrane; Plasma membrane] Integral membrane protein 2B, a type II integral membrane protein; gene mutation is associated with familial British and Danish dementias, which are characterized by amyloid plaque deposits, neurofibrillary tangles, and neuronal loss El-Agnaf, O. M. et al. Biochemistry 40, 3449-57 (2001). Holton, J. L. et al. Am J Pathol 158, 515-26 (2001).
		583443 Itm2b	1.2E-77	[Mus musculus][Unspecified membrane] Integral membrane protein 2B, a type II integral membrane protein; human ITM2B mutation is associated with familial British and Danish dementias, which are characterized by amyloid plaque deposits, neurofibrillary tangles, and neuronal loss Pittois, K. et al. Gene 217, 141-9 (1998).
22	7512447CD1	g14149046	2.6E-67	[Drosophila melanogaster] turtle protein, isoform 2 Bodily, K. D. et al. Neuroscience. 21, 3113-3125 (2001)

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO: or PROTEOME ID NO:	Probability Score	Annotation
22 cont		590029 Dcc	2.4E-28	[Rattus norvegicus][Receptor (signalling)][Plasma membrane] Deleted in colorectal cancer, netrin 1 receptor, member of the immunoglobulin-CAM family which mediates axon guidance and regulates apoptosis; human DCC is deleted in colorectal cancers Zou, Y. et al. Cell 102, 363-75 (2000). Stein, E. et al. Science 291, 1976-82 (2001).
		742836 DSCAM	3.6E-20	[Homo sapiens][Adhesin/agglutinin][Plasma membrane] Down syndrome cell adhesion molecule, a member of the immunoglobulin superfamily, expressed primarily in the brain Agarwala, K. L. et al. Brain Res Mol Brain Res 79, 118-26 (2000). Yamakawa, K. et al. Hum Mol Genet 7, 227-37 (1998).

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	7506758CD1	151	Phorbol esters / diacylglycerol binding domain: C63-K127	PROFILESCAN
			Potential Phosphorylation Sites: S84 T31 T36 T54 Y121	MOTIFS
2	4381669CD1	2507	Spectrin repeat: Q2150-D2257, L1062-S1163, G1819-R1923, N1491-E1593, E732-S837, K505-Q614, V1596-E1707, S1408-E1488, S872-Q940, L1166-S1271, R1710-H1816, E704-G729, T2120-Q2147	HMMER_PFAM
			Spectrin repeat proteins PF00435: F1403-A1431, W1577-K1592, L1993-A2012 P < 0.0052	BLIMPS_PFAM
			Potential Phosphorylation Sites: S63 S86 S176 S209 S266 S286 S299 S328 S329 S402 S448 S471 S473 S523 S564 S592 S634 S688 S694 S697 S733 S735 S837 S844 S943 S1348 S1369 S1408 S1410 S1434 S1454 S1480 S1497 S1564 S1607 S1720 S1729 S1788 S1849 S1933 S1977 S1980 S2015 S2039 S2079 S2092 S2096 S2246 S2291 S2321 S2375 S2383 S2384 S2398 S2429 S2437 S2446 S2478 T102 T296 T314 T490 T586 T721 T746 T813 T922 T980 T1005 T1098 T1155 T1170 T1177 T1313 T1402 T1508 T1673 T1708 T1765 T1808 T1826 T1836 T1843 T2072 T2169 T2220 T2408 Y396 Y1128 Y1295 Y1568	MOTIFS
			Potential Glycosylation Sites: N294 N681 N710 N1604 N1781 N1966	MOTIFS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3	7503554CD1	375	Cell attachment sequence: R256-D258 signal_cleavage: M1-A22 Signal Peptide: M4-A22, M1-A22 Leucine Rich Repeat: N261-L284, N213-E236, N93-P116, D310-P334, N237-V260, N189-I212, H285-P309, N141-H164, N165-P188, Q117-S140 Leucine rich repeat N-terminal domain: D28-P68 Leucine-rich repeat signature PR00019: L94-V107, L139-L152 PROTEIN BAC CLONE RG118D07 FROM 7Q31 COMPLETE SEQUENCE GLIOMA AMPLIFIED PD032016: M283-L349 PROTEIN BAC CLONE RG118D07 FROM 7Q31 COMPLETE SEQUENCE NEURONAL LEUCINERICH PD080235: P188-E236 BAC CLONE RG118D07 FROM 7Q31 COMPLETE SEQUENCE GLIOMA AMPLIFIED ON PD080342: N237-N282 Potential Phosphorylation Sites: S51 S173 S242 T42 T95 Potential Glycosylation Sites: N93 N103 N223	MOTIFS SPSCAN HMMER HMMER_PFAM HMMER_PFAM BLIMPS_PRINTS BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM MOTIFS MOTIFS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
	ID		Cell attachment sequence: R277-D279	MOTIFS
4	7506077CD1	340	<p>CLN3 protein: L99-S340, M1-A98</p> <p>Cytosolic domains: M1-N37, T134-G182, R240-R245, H296-R307</p> <p>Transmembrane domains: A38-H60, T114-L133, L183-F205, Q220-L239, F246-G268, I273-F295, E308-L330</p> <p>Non-cytosolic domains: D61-Q113, E206-Q219, F269-S272, P331-S340</p> <p>PROTEIN TRANSMEMBRANE CLN3 BTN1 BTNIP BATTEN'S DISEASE NEURONAL CEROID LIPOFUSCINOSIS PD007801: D140-L339, D13-S135, A98-K164</p> <p>CLN3 PROTEIN TRANSMEMBRANE BATTEN'S DISEASE NEURONAL CEROID LIPOFUSCINOSIS MUTATION PD156246: M1-K36</p> <p>CLN3; DISEASE; BATTEN; DM05338 A57219 83-438: A98-S340, P83-L124</p> <p>DM05338 P47040 1-407: Y186-Q338, F41-L63</p> <p>Potential Phosphorylation Sites: S7 S12 S14 S64 S69 S73 S87 S88 S172 S238 T19 T134 T302</p>	<p>HMMER_PFAM</p> <p>TMHMMER</p> <p>BLAST_PRODOM</p> <p>BLAST_PRODOM</p> <p>BLAST_DOMO</p> <p>MOTIFS</p>

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5	7506765CD1	287	<p>Potential Glycosylation Sites: N49 N71 N85 N212 signal_cleavage: M1-A15 Signal Peptide: M1-A20, M1-A21, M1-H22 C1q domain: A160-L284 Collagen triple helix repeat (20 copies): G76-G135 C1q domain proteins BL01113: G85-S111, V174-I209, D243-K262, S277-P286 Lysosome-associated membrane glycoproteins signatures: E145-L175</p> <p>Complement C1Q domain signature PR00007: P168-K194, F195-G214, D243-D264, K275-Y285 PRECURSOR SIGNAL COLLAGEN REPEAT HYDROXYLATION GLYCOPROTEIN CHAIN PLASMA EXTRACELLULAR MATRIX PD002992: P168-L284 COLLAGEN ALPHA PRECURSOR CHAIN REPEAT SIGNAL CONNECTIVE TISSUE EXTRACELLULAR MATRIX PD000007: A39-G118, P72-G118, P35-D110 PRECOLLAGEN P PRECURSOR SIGNAL PD072959: A38-G118, P40-P117 PROCOLLAGEN, TYPE XVII, ALPHA 1 BULLOUS PEMPHIGOID AUTOANTIGEN BP180 COLLAGEN XVII ANTIGEN CELL ADHESION PD071338: P44-G112 C1Q DOMAIN :DM00777 S23297 465-674: P84-L283, P69-G213; DM00777 P23206 477-673: G94-P286; DM00777 P02746 70-250: G82-D287; DM00777 P27658 551-743: G88-P286 Potential Phosphorylation Sites: S111 S142 S167 S255 T28 T192</p>	<p>MOTIFS SPSCAN HMMER HMMER_PFAM HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLIMPS_PRINTS BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_DOMO MOTIFS</p>

Table 3

SEQ ID NO:	Incye Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
6	7490048CD1	1048	<p>C1q domain signature: F177-Y207</p> <p>PDZ domain (Also known as DHR or GLGF): T661-Q742, H562-D645, D153-D238, V53-E135, E461-D549, M253-V336, K946-K1027</p> <p>PDZ domain proteins (Also known as DHR or GLGF) PF00595: I702-N712</p> <p>PROTEIN SH3 DOMAIN REPEAT PD00289: G705-G718</p> <p>AMPA Receptor Protein PD084959: P335-T460; PD065834: A845-P1040; PD176166: I279-L334; PD117239: L748-Y840</p> <p>Potential Phosphorylation Sites: S5 S43 S197 S272 S288 S314 S324 S326 S339 S369 S422 S499 S570 S581 S597 S676 S715 S754 S759 S787 S795 S839 S848 S929 S961 S1025 S1033 S1044 T52 T72 T223 T308 T525 T691 T736 T817 T843 T940 T975 Y23 Y134 Y157</p>	<p>MOTIFS</p> <p>HMMER_PFAM</p> <p>BLIMPS_PFAM</p> <p>BLIMPS_PRODROM</p> <p>BLAST_PRODROM</p> <p>MOTIFS</p>
7	2133585CD1	419	<p>Potential Glycosylation Sites: N247 N275 N713</p> <p>Signal cleavage: M1-S30</p> <p>Signal Peptide: H6-S30, M1-S30, L13-S30, P8-S30</p> <p>HYR (hyalin repeat) domain: V175-V257</p> <p>Sushi domain (SCR repeat): C57-C115, C262-C317, C120-C174</p> <p>Sushi domain proteins (S PF00084): C69-Q73, N140-Y151, L308-C317</p> <p>PROTEIN SUSHI REPEATCONTAINING SRPX PRECURSOR SIGNAL REPEAT SUSHI REPEAT POLYMORPHISM ALTERNATIVE PD020056: V25-S311; PD019555: V175-R261; PD021630: A318-L403</p>	<p>MOTIFS</p> <p>SPSCAN</p> <p>HMMER</p> <p>HMMER_PFAM</p> <p>HMMER_PFAM</p> <p>BLIMPS_PFAM</p> <p>BLAST_PRODROM</p>

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			SUSHI REPEAT DM04887 P33730 1-610: G65-E189, K63-M320, G65-C174, Y282-A319, R261-C317; P1658 1-609: G45-M320, L14-Y51 P27113 1-551: G45-C317, C57-C174, G65-V187, R258-V326, G381-L416 Potential Phosphorylation Sites: S37 S105 S110 S141 S168 S173 S186 S277 S311 T83 T152 T160 T198 T240 T250 T349 T375 T409 Y138 Y282	BLAST_DOMO
8	7509063CD1	1109	Spectrin repeat: T722-Q749, Q752-D859, G397-R501, N69-E171, V174-E285, R2-E66, R288-H394 Potential Phosphorylation Sites: S12 S32 S58 S75 S142 S185 S298 S307 S366 S427 S512 S556 S559 S594 S641 S681 S694 S698 S848 S893 S923 S977 S985 S986 S1000 S1031 S1039 S1048 S1080 T86 T251 T286 T343 T386 T404 T414 T421 T636 T674 T771 T822 T1010 Y146 Potential Glycosylation Sites: N182 N359 N545 N635	MOTIFS HMMER_PFAM
9	5496710CD1	1308	Signal Peptide: M1-A25 EGF-like domain: C553-C585, C962-C996, R552-H586, H961-S997 F5/8 type C (coagulation-associated) domain: P34-V174, D30-C177 Laminin G domain: L813-M940, I204-V341, E390-K524, S1038-V1176, F821-D943, F398-D527, F212-I344, N1073-S1131 Cytosolic domain: Y1265-F1308 Transmembrane domain: V1242-I1264 Non-cytosolic domain: M1-A1241	MOTIFS HMMER HMMER_PFAM HMMER_PFAM HMMER_PFAM HMMER_PFAM TMHMMER

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			PROTEIN NEUREXIN IV CONTACTIN ASSOCIATED PD013624: C558-V817; PD022248: S818-S1030; PD022247: V341-S550	BLAST_PRODUM
			W03D8.6 PROTEIN GLYCOPROTEIN PD185819: F928-S1169, C785-D983, G511-G601, S396-S535, I208-G314	BLAST_PRODUM
			DISCOIDIN I N-TERMINAL DM00516 A42580 2085-2210: P56-C177; DM00516 P12259 2095-2223: P56-C177 DM00516 P21956 338-462: P56-C177; DM00516 P00451 2221-2347: P56-C177	BLAST_DOMO
			Potential Phosphorylation Sites: S46 S75 S149 S209 S265 S376 S387 S459 S522 S550 S588 S715 S1045 S1131 S1150 S1186 S1218 T287 T647 T769 T896 T1048 T1211 T1225 Y711 Y778	MOTIFS
			Potential Glycosylation Sites: N260 N285 N359 N538 N574 N602 N625 N637 N706 N748 N1023 N1073	MOTIFS
			Cell attachment sequence: R786-D788	MOTIFS
			ATP/GTP-binding site motif A (P-loop): G314-S321	MOTIFS
			Coagulation factors 5/8 type C domain (FA58C) signature 1: G69-G98	MOTIFS
			Coagulation factors 5/8 type C domain (FA58C) signature 2: P159-C177	MOTIFS
			Leucine zipper pattern: L407-L428	MOTIFS
10	72150826CD1	1009	Signal_cleavage: M1-S24	SPSCAN
			Signal Peptide: M1-S17, M1-G19, M1-G21, M1-A22, M1-S24, M1-R26	HMMER
			EGF-like domain: C569-C601, C788-C819, C347-C380	HMMER_PFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			Fibronectin type III domain: P142-S228, V35-S126	HMMER_PFAM
			Laminin G domain: F415-D546, F641-H770, F860-1980	HMMER_PFAM
			Cytosolic domain: M1-G6	TMHMMER
			Transmembrane domain: V7-I29	
			Non-cytosolic domain: R30-K1009	
			Type II EGF-like signature PR00010: D560-E571, G598-F605, D586-F596, K597-D603	BLIMPS_PRINTS
			NEUREXIN; ALPHA; III; CYSTEINE;	BLAST_DOMO
			DM00060[Q05793]3542-3652: K861-G960, M635-G738	
			DM00060[P98160]4227-4338: M858-G960, E638-G738, I411-A515	
			DM00060[Q05793]3004-3118: Y631-G738, Y406-G514	
			DM00060[Q05793]3265-3373: M635-V739, Y406-G514, M858-M961	
			Potential Phosphorylation Sites:	MOTIFS
			S24 S80 S127 S154 S161 S191 S225 S244 S273 S294 S298 S379	
			S557 S615 S633 S749 S798 S850 S911 S928 S992 T96 T190 T505	
			T527 T640 T703 T863 T932 T940 T968	
			Potential Glycosylation Sites: N47 N909	MOTIFS
			Cell attachment sequence: R434-D436, R872-D874	MOTIFS
			EGF-like domain signature 1: C369-C380, C590-C601, C808-C819	MOTIFS
			EGF-like domain signature 2: C590-C601, C808-C819	MOTIFS
11	6799476CD1	962	Signal_cleavage: M1-A28	SPSCAN
			Signal Peptide:	HMMER
			A10-A28, L9-A28; P7-A28, M1-G24, M1-A28, P11-A28, P5-A28, P7-A28	
			Cadherin domain: Y169-K258, Y42-N155	HMMER_PFAM
			Cytosolic domain: R864-Y962	TMHMMER
			Transmembrane domain: A841-I863	
			Non-cytosolic domain: M1-T840	

Table 3

SEQ ID NO:	Incye Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			Potential Phosphorylation Sites: S104 S145 S168 S256 S320 S381 S408 S483 S493 S527 S554 S649 S732 S748 S765 S819 S904 S905 S934 T47 T172 T222 T238 T248 T291 T318 T403 T477 T524 T541 T607 T684 T741 T870 T876 T898 T927 Y42 Y227 Y319 Y540	MOTIFS
			Potential Glycosylation Sites: N346 N366 N946	MOTIFS
12	7509488CD1	953	Signal_cleavage: M1-A29	SPSCAN
			Signal Peptide: P11-A29, V10-A29, R8-A29, P5-A29, M1-A29, P12-A29	HMMER
			Cadherin domain: Y160-K249, Y43-N146	HMMER_PFAM
			Cytosolic domain: R855-Y953	TMHMMER
			Transmembrane domain: A832-I854	
			Non-cytosolic domain: M1-T831	
			Potential Phosphorylation Sites: S95 S136 S159 S247 S311 S372 S399 S474 S484 S518 S545 S640 S723 S739 S756 S810 S895 S896 S925 T48 T163 T213 T229 T239 T282 T309 T394 T468 T515 T532 T598 T675 T732 T861 T867 T889 T918 Y43 Y218 Y310 Y531	MOTIFS
			Potential Glycosylation Sites: N337 N357 N937	MOTIFS
13	7510060CD1	582	Signal Peptide: M1-G23, M1-G19	HMMER
			I type Ig domains from SCOP: P239-P329, V331-L416	HMMER_INCY
			Ig superfamily from SCOP: K328-L415, I242-L320, T140-P239	HMMER_INCY
			Immunoglobulin: N332-E410, N246-M323, P27-L135, V144-K237	HMMER_SMART
			Immunoglobulin C-2 Type: I252-G312, V338-G399	HMMER_SMART
			Immunoglobulin domain: G340-A394, G254-A307, G35-Y116	HMMER_PFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			Cytosolic domain: T534-H582 Transmembrane domain: W511-I533 Non-cytosolic domain: M1-M510	TMHMMER
			GLYCOPROTEIN ANTIGEN PRECURSOR PD02327: L259-L280	BLIMPS_PRODOME
			GLYCOPROTEIN PRECURSOR MYELIN CELL ADHESION TRANSMEMBRANE SIGNAL IMMUNOGLOBULIN FOLD MYELIN ASSOCIATED PD017076: E395-E580	BLAST_PRODOME
			CELL PRECURSOR GLYCOPROTEIN TRANSMEMBRANE SIGNAL IMMUNOGLOBULIN FOLD ADHESION ALTERNATIVE SPLICING PD005007: L7-E229	BLAST_PRODOME
			do MYELIN; SCHWANN; SIALOADHESIN; FORM; DM03744 P20917 I-138: M1-N139 DM03744 H0593 I-137: M1-I137	BLAST_DOMO
			IMMUNOGLOBULIN DM00001 P20917 I40-234: T140-D235 DM00001 P20917 323-407: Y238-S408	BLAST_DOMO
			Potential Phosphorylation Sites: S31 S133 S247 S351 S383 S436 S456 S463 S549 S577 T128 T153 T296 T452 T475 T489 T536	MOTIFS
			Potential Glycosylation Sites: N99 N223 N246 N315 N332 N406 N450 N454 N541	MOTIFS
			Cell attachment sequence: R118-D120 signal_cleavage: M1-C17	MOTIFS SPSCAN
14	7510226CD1	188	Signal Peptide: M2-A24	HMMER
			ZP domain proteins BL00682: S15-G21	BLIMPS_BLOCKS
			Ribosomal protein S15 signature: Q73-G144	PROFILES CAN
			Potential Phosphorylation Sites: S16	MOTIFS
			REPEAT PROTEIN STRIATIN WD CALMODULIN BINDING CELL CYCLE NUCLEAR AUTOANTIGEN SG2NA S/G2 PD011690: T57-R179	BLAST_PRODOME

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
15	7510385CD1	478	signal_cleavage: M1-A24 Signal Peptide: M1-G22, M1-A24, M1-S27 Sema domain: Y55-R308 Cytosolic domain: M1-A4 Transmembrane domain: G5-S27 Non-cytosolic domain: P28-R478	SPSCAN HMMER HMMER_PFAM TMHMMER
			SEMAPHORIN PROTEIN PRECURSOR RECEPTOR KINASE SIGNAL TYROSINE TYROSINEPROTEIN FAMILY HEPATOCYTE PD001844: Y55-E183, E162-G311 SEMAPHORIN V A PRECURSOR SEM SIGNAL IMMUNOGLOBULIN FOLD MULTIGENE FAMILY PD022826: M1-C54	BLAST_PRODOM BLAST_PRODOM
			do SEMAPHORIN; FASCICLIN; COLLAPLIN; II; DM01606 48744 1-639: M1-E309 DM01606 48747 1-646: G5-E309 DM01606 49069 1-646: G5-E309 DM01606 48748 1-589: A6-E309	BLAST_DOMO
			Potential Phosphorylation Sites: S34 S84 S168 S209 S321 S327 T249 T302	MOTIFS
			Potential Glycosylation Sites: N82 N124	MOTIFS
16	7511618CD1	412	UBA/TS-N domain: R369-S409 Ubiquitin associated domain: F370-G408 F15C11.2 PROTEIN, Ubiquitin family (<i>C. elegans</i>) PD183489: V58-P330	HMMER_PFAM HMMER_SMART BLAST_PRODOM
			Potential Phosphorylation Sites: S83 S127 S135 T40 T43 T329 T395	MOTIFS
			Potential Glycosylation Sites: N55 N125 N324 LGN motif, putative GEF specific for G-alpha: M63-V85, Q23-L45	MOTIFS HMMER_PFAM
17	6244135CD1	136		

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			LGN motif, putative GEFs specific for G-alpha: M63-V85, Q23-L45	HMMER_SMART
			signal_cleavage: M38-S96	SPSCAN
			PURKINJE CELL PROTEIN 2 PCD5 CELL SPECIFIC L7	BLAST_PRODOR
			NEURONE PD067101: M38-P136	
			Potential Phosphorylation Sites: S55 S65 S127 T52 T114	MOTIFS
18	7506689CD1	198	signal_cleavage: M1-G34	SPSCAN
			Signal Peptide: M1-G34	HMMER
			Potential Phosphorylation Sites: S33 S48 S153 S178	MOTIFS
			Potential Glycosylation Sites: N64	MOTIFS
19	7510185CD1	813	signal_cleavage: M1-G35	SPSCAN
			Signal Peptide: P18-G35	HMMER
			Signal Peptide: L16-G35	HMMER
			Signal Peptide: P13-G35	HMMER
			Signal Peptide: R11-G35	HMMER
			Signal Peptide: M1-G35	HMMER
			Signal Peptide: A14-G35	HMMER
			Signal Peptide: P13-G37	HMMER
			Fibronectin type 3 domain: P424-S507, A521-G603	HMMER_SMART
			Immunoglobulin: P336-L418, P244-Q327, P145-S228, P48-A136	HMMER_SMART
			Immunoglobulin C-2 Type: P342-G407, V54-G124, E151-S216, T250-T314	HMMER_SMART
			Fibronectin type III domain: P424-S510, A521-T606	HMMER_PFAM
			Immunoglobulin domain: G344-A402, H252-A309, G56-A119, G153-A211	HMMER_PFAM
			I type Ig domains from SCOP: H335-G425, K236-F332, E41-D140	HMMER_INCY
			Ig superfamily from SCOP: F332-L423, F141-G231, I240-A330, F44-I133	HMMER_INCY

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			Cytosolic domain: G662-Q813 Transmembrane domain: T639-F661 Non-cytosolic domain: M1-T638	TMHMMER
			NEURONAL CELL ADHESION MOLECULE PUNC PD123980: N604-L621 T639-A803	BLAST_PRODOM
			BASIC FIBROBLAST GROWTH FACTOR RECEPTOR I DM01287/A39752 I-814: L16-V118 P244-E421 DM01287/P16092 I-821: W17-G124 P244-A420 DM01287/A39752 I-814: Q134-V210	BLAST_DOMO
			IMMUNOGLOBULIN DM00001/P43146 328-410: P329-Q410	BLAST_DOMO
			Potential Phosphorylation Sites: S8 S108 S128 S216 S272 S412 S436 S443 S486 S528 S582 S611 S616 S685 T74 T137 T148 T181 T502 T517 T606	MOTIFS
			Potential Glycosylation Sites: N93 N246 N381 N382 N580 N604 N634	MOTIFS
20	1420867CD1	165	FER1 PD185307: M1-Q125	BLAST_PRODOM
			Potential Phosphorylation Sites: S101 S106 T96	MOTIFS
21	7512289CD1	229	Cytosolic domain: M1-R51 Transmembrane domain: A52-Y74 Non-cytosolic domain: L75-S229	TMHMMER
			PROTEIN INTEGRAL MEMBRANE TRANSMEMBRANE SIGNAL ANCHOR 2A E25 2B E316 E25B PD023945: M1-L156, P108-C228	BLAST_PRODOM
			Potential Phosphorylation Sites: S22 T114 T169 T191 T199 Y192	MOTIFS
22	7512447CD1	1163	signal_cleavage: M1-G17	SPSCAN
			Signal Peptide: M1-G17	HMMER
			Signal Peptide: M1-G20	HMMER
			Signal Peptide: M1-G22	HMMER

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			Fibronectin type 3 domain: L608-F687, P492-G577	HMmer_SMART
			Immunoglobulin: P143-L224, P233-L320, V26-T131, P408-L488	HMmer_SMART
			Immunoglobulin C-2 Type: Q149-G213, E415-A477, N239-L308, R32-Q115	HMmer_SMART
			Fibronectin type III domain: P492-S580, L608-S692	HMmer_PFAM
			Immunoglobulin domain: L151-A208, G417-A472, S241-P303, I326-P381, G34-V110	HMmer_PFAM
			I type Ig domains from SCOP: P135-L224, G225-I326, A400-V495	HMmer_INCY
			Ig superfamily from SCOP: Q139-P227, I229-P310, I405-V494, S312-F404, G22-F138	HMmer_INCY
			Cytosolic domain: N745-L1163	TMHMMER
			Transmembrane domain: G722-L744	
			Non-cytosolic domain: M1-A721	
			Potential Phosphorylation Sites: S74 S209 S285 S585 S700 S797 S819 S850 S960 S1010 S1044 S1059 S1065 S1092 T155 T169 T190 T291 T619 T661 T768 T942 T987 T1064 T1107 T1120 Y106	MOTIFS
			Potential Glycosylation Sites: N124 N188 N235 N239 N256 N452 N497 N508 N696 N1063	MOTIFS

Table 8

SEQ ID NO:	PID	EST ID	SNP ID	EST SNP	CB1 SNP	EST Allele	Allele 1	Allele 2	Amino Acid	Caucasian Allele 1 frequency	African Allele 1 frequency	Asian Allele 1 frequency	Hispanic Allele 1 frequency
28	7490048	3762473H1	SNP00109796	234	854	T	T	C	L252	0.73	n/a	n/a	n/a
29	2133585	2552009H1	SNP00002569	149	1811	G	G	C	noncoding	n/a	n/a	n/a	n/a
30	7509063	5641659H1	SNP00012015	242	3092	C	C	T	S995	0.90	n/d	n/d	0.97
31	5496710	5450982H1	SNP00008406	167	4138	G	A	G	noncoding	n/a	n/a	n/a	n/a
32	72150826	3349030H1	SNP00028258	132	2700	C	C	A	P839	n/a	n/a	n/a	n/a
33	6799476	1667323H1	SNP00003249	208	817	T	C	T	V213	n/a	n/a	n/a	n/a
34	7509488	1667323H1	SNP00003249	208	789	T	C	T	V204	n/a	n/a	n/a	n/a
35	7510060	7091751H1	SNP00027969	189	1003	G	G	A	L289	n/d	n/d	n/d	n/d
37	7510385	181454H1	SNP00016645	144	910	G	G	C	W283	n/d	n/d	n/d	n/d
38	7511618	2246326H1	SNP00003003	219	1301	G	G	A	S321	0.86	n/d	0.97	0.99
40	7506689	2504535H1	SNP00154755	36	2242	T	T	C	noncoding	n/a	n/a	n/a	n/a
41	7510185	4710260H1	SNP00112063	200	2248	G	T	G	V750	0.45	0.35	0.77	0.45
43	7512289	085202H1	SNP00112417	14	298	C	C	A	P31	n/a	n/a	n/a	n/a
44	7512447	2810195T6	SNP00006851	158	3802	A	A	G	noncoding	n/a	n/a	n/a	n/a

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
23/7506758CB1/ 2208	1-601, 189-595, 189-600, 280-600, 316-586, 316-852, 316-857, 316-1977, 344-600, 489-1165, 599-952, 600-671, 603-1225, 616-1183, 684-1284, 705-1159, 716-1207, 730-1014, 736-793, 757-1049, 772-1374, 861-1105, 861-1122, 864-1119, 877-1113, 892-1166, 893-1163, 1101-1385, 1190-1423, 1215-1474, 1231-1487, 1452-1959, 1531-1765, 1533-1976, 1550-1978, 1565-1975, 1633-1928, 1665-1967, 1706-1939, 1708-1914, 1708-1943, 1708-1985, 1741-1972, 1838-1951, 1927-2208, 1975-2173, 1975-2203, 1975-2208, 1985-2076, 1986-2208, 2000-2203, 2149-2208
24/4381669CB1/ 7611	1-321, 227-715, 237-498, 247-723, 275-701, 278-671, 281-697, 286-708, 287-688, 298-875, 298-878, 298-884, 300-679, 309-702, 311-704, 313-698, 320-602, 323-642, 324-626, 329-608, 343-592, 362-701, 374-602, 402-953, 427-712, 491-592, 526-1041, 619-1364, 783-1400, 832-1389, 964-1181, 980-1353, 1086-1448, 1131-1413, 1173-1436, 1207-1850, 1237-1438, 1401-1661, 1415-1532, 1444-1643, 1450-2113, 1543-1613, 1611-3712, 1807-2435, 1929-2435, 2029-2435, 2138-2435, 2277-2397, 2284-2863, 2314-2863, 3291-3666, 3297-3666, 3333-3490, 3471-3858, 3559-3810, 3571-3650, 3808-7611
25/7503554CB1/ 2259	1-599, 1-628, 1-652, 1-666, 1-697, 1-749, 1-771, 1-817, 1-861, 1-875, 1-2214, 22-282, 22-586, 22-587, 22-615, 65-346, 88-616, 96-777, 102-361, 102-371, 107-651, 107-652, 134-673, 153-402, 175-607, 179-868, 190-841, 291-550, 320-707, 334-635, 334-766, 356-870, 385-874, 388-673, 403-1050, 435-678, 448-1105, 473-783, 473-785, 474-688, 481-822, 488-982, 513-816, 513-827, 515-1168, 546-946, 561-988, 578-851, 584-835, 584-1082, 593-1235, 597-871, 654-1347, 656-928, 658-1296, 725-1423, 742-1409, 743-1423, 766-905, 771-1022, 773-1400, 782-1365, 790-1129, 800-1044, 824-1082, 832-1475, 844-1108, 848-1371, 871-1508, 872-1424, 894-1521, 902-1540, 918-1426, 919-1231, 919-1570, 934-1431, 938-1547, 983-1514, 984-1629, 989-1532, 1007-1601, 1023-1589, 1053-1571, 1057-1707, 1157-1907, 1178-1965, 1185-1494, 1185-1667, 1216-1469, 1290-1556, 1293-1545, 1320-1801, 1321-1773, 1322-1722, 1335-1563, 1358-1953, 1362-1595, 1373-1649, 1403-2205, 1411-2187, 1415-2189, 1415-2203, 1422-1710, 1445-2127, 1455-2083, 1468-1713, 1481-2148, 1495-1785, 1533-1786, 1533-1797, 1533-2116, 1566-2148, 1567-2160, 1577-2053, 1581-2226, 1582-2196, 1585-2155, 1588-2133, 1595-1837, 1606-2157, 1608-1852, 1631-2042, 1653-2159, 1666-2146, 1667-2207, 1691-2159, 1694-2159, 1704-2147, 1718-2159, 1731-2146, 1758-2146, 1773-2042, 1774-2147, 1782-2146, 1783-2146, 1795-2136, 1796-2049, 1805-2159, 1808-2159, 1811-2035, 1838-2140, 1842-2146, 1864-2150, 1873-2149, 1886-2259, 1931-2146, 1963-2253, 1977-2184, 1996-2259, 2051-2258

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
26/7506077CBI/ 1522	<p>1-248, 1-250, 1-1522, 6-268, 12-264, 55-543, 70-350, 72-337, 73-379, 74-340, 74-479, 74-526, 74-546, 78-295, 78-311, 78-349, 79-315, 79-370, 106-398, 123-392, 123-395, 144-413, 177-309, 177-378, 177-394, 177-403, 177-409, 177-410, 177-415, 177-422, 177-427, 177-433, 177-445, 177-447, 177-454, 177-455, 177-479, 177-540, 178-407, 178-513, 178-660, 178-684, 178-699, 178-746, 178-810, 181-300, 181-411, 189-334, 192-730, 194-392, 200-517, 204-906, 223-490, 225-493, 226-547, 229-812, 239-351, 261-547, 295-545, 300-419, 316-507, 318-547, 377-532, 379-547, 491-817, 514-657, 545-720, 554-1106, 556-1138, 557-1064, 564-1231, 568-848, 578-1087, 583-1304, 588-861, 595-1204, 601-1121, 614-1096, 615-1102, 617-1195, 623-1037, 625-904, 628-800, 632-1255, 646-852, 651-847, 656-917, 662-1032, 663-903, 669-1284, 679-1261, 690-970, 707-1192, 712-1263, 715-818, 723-1108, 734-1033, 736-1318, 742-996, 757-988, 758-1522, 776-1036, 787-1078, 796-1441, 799-1364, 802-1085, 812-1008, 813-1064, 813-1070, 813-1436, 831-1294, 832-1261, 833-1456, 835-1102, 837-1505, 842-1084, 851-1113, 851-1522, 852-1144, 854-1080, 860-1110, 866-1121, 866-1162, 866-1513, 867-1106, 867-1167, 868-1105, 869-1151, 884-1075, 884-1442, 889-1243, 895-1508, 904-1462, 905-1062, 907-1145, 909-1097, 912-1522, 915-1291, 919-1433, 922-1396, 924-1506, 926-1441, 926-1501, 928-1522, 931-1475, 938-1201, 948-1522, 966-1522, 972-1345, 977-1301, 977-1522, 979-1253, 984-1187, 984-1522, 986-1522, 987-1508, 988-1265, 989-1522, 990-1509, 993-1141, 1012-1522, 1013-1265, 1015-1344, 1016-1301, 1017-1125, 1017-1276, 1017-1522, 1019-1521, 1023-1520, 1027-1456, 1028-1231, 1035-1279, 1037-1295, 1037-1301, 1044-1522, 1045-1314, 1045-1522, 1047-1311, 1047-1506, 1047-1522, 1048-1522, 1049-1292, 1051-1226, 1052-1331, 1054-1522, 1056-1513, 1057-1522, 1058-1356, 1060-1522, 1062-1516, 1063-1522, 1069-1511, 1072-1522, 1074-1286, 1074-1511, 1080-1362, 1081-1522, 1084-1513, 1087-1369, 1092-1406, 1093-1513, 1093-1522, 1102-1274, 1103-1513, 1106-1522, 1109-1371, 1109-1504, 1109-1519, 1110-1306, 1110-1352, 1111-1514, 1112-1513, 1115-1469, 1118-1514, 1126-1522, 1130-1518, 1134-1351, 1144-1514, 1145-1513, 1149-1513, 1154-1513, 1155-1518, 1156-1422, 1157-1522, 1162-1516, 1163-1415, 1164-1509, 1166-1512, 1168-1512, 1168-1513, 1168-1514, 1168-1516, 1172-1522, 1174-1508, 1175-1442, 1176-1513, 1179-1513, 1180-1513, 1182-1511, 1184-1513, 1186-1522, 1187-1512, 1196-1516, 1208-1513, 1208-1516, 1213-1443, 1218-1467, 1220-1514, 1221-1414, 1222-1517, 1223-1474, 1228-1365, 1230-1513, 1233-1513, 1235-1353, 1235-1512, 1237-1441, 1238-1512, 1238-1513, 1242-1441, 1250-1522, 1254-1513, 1261-1514, 1282-1513, 1287-1410, 1292-1515, 1301-1516, 1317-1520, 1328-1520, 1364-1522, 1397-1522, 1413-1522, 1416-1513, 1428-1514</p>

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
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28/7490048CB1/ 3311	1-254, 1-3244, 155-501, 155-591, 155-606, 155-641, 155-798, 342-505, 342-507, 403-1105, 542-823, 542-869, 542-996, 542-1089, 542-1142, 542-1145, 556-1145, 560-827, 560-999, 667-827, 695-1103, 739-810, 803-1145, 878-1145, 888-1145, 896-1085, 902-1145, 1015-1145, 1039-1145, 1040-2514, 1044-1145, 1046-1145, 1097-1145, 1359-1623, 2689-2753, 2689-3311, 2972-3311, 3098-3311, 3180-3311
29/2133585CB1/ 1874	1-187, 1-271, 1-508, 13-330, 147-815, 304-740, 306-747, 387-855, 393-807, 409-898, 410-898, 432-1045, 547-1218, 604-1241, 615-1874, 634-1289, 637-1254, 681-1207, 730-1442, 779-1356, 791-1364, 796-1364, 810-1448, 812-1227, 824-1296, 844-1320, 855-1287, 857-1370, 887-1363, 902-1344, 930-1420, 930-1430, 1001-1422, 1013-1631, 1051-1433, 1079-1586, 1085-1573, 1410-1874
30/7509063CB1/ 4211	1-232, 1-278, 1-495, 1-4187, 134-733, 203-754, 217-511, 269-935, 311-1123, 394-937, 425-553, 471-929, 482-1158, 520-984, 591-1034, 685-953, 685-1253, 685-1293, 746-1336, 760-1397, 839-1423, 918-1135, 961-1536, 968-1493, 968-1558, 994-1635, 1007-1686, 1095-1669, 1131-1727, 1236-1463, 1360-2012, 1394-1704, 1396-1928, 1397-1693, 1418-1901, 1444-1609, 1477-1986, 1477-2002, 1478-2134, 1536-2068, 1538-1710, 1538-1934, 1583-1856, 1653-2099, 1774-2299, 1836-2374, 1898-2190, 1911-2643, 1955-2517, 2011-2204, 2011-2489, 2011-2516, 2011-2594, 2011-2601, 2061-2238, 2069-2593, 2078-2351, 2101-2361, 2112-2432, 2147-2887, 2168-2599, 2176-2418, 2199-2473, 2212-2950, 2218-2333, 2234-2811, 2237-2875, 2244-2851, 2245-2773, 2295-2537, 2297-2548, 2346-2993, 2351-2682, 2353-3000, 2356-2795, 2389-2915, 2393-2658, 2397-2785, 2402-2687, 2422-2701, 2427-3029, 2434-3089, 2440-3079, 2468-3025, 2474-2922, 2477-2698, 2486-3059, 2491-2781, 2492-2724, 2492-3033, 2503-2760, 2525-2664, 2531-2760, 2545-3390, 2549-2991, 2558-2802, 2563-3283, 2618-2856, 2634-2903, 2636-2851, 2641-3469, 2645-2979, 2646-2905, 2693-3046, 2713-2978, 2725-3173, 2740-3354,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
30 cont	<p>2759-3047, 2759-3237, 2775-3262, 2779-3064, 2779-3075, 2798-3029, 2799-3389, 2806-3026, 2806-3074, 2806-3087, 2806-3155, 2820-3118, 2820-3151, 2823-2961, 2826-3104, 2834-3087, 2837-3115, 2849-3196, 2850-3114, 2853-3025, 2853-3448, 2856-3090, 2858-3090, 2868-3434, 2890-3405, 2899-3134, 2902-3099, 2902-3150, 2911-3205, 2912-3166, 2915-3137, 2916-3529, 2917-3396, 2938-3212, 2944-3384, 2944-3599, 2946-3218, 2956-3217, 2961-3446, 2967-3200, 2983-3253, 2999-3629, 2999-3636, 3012-3218, 3023-3278, 3030-3306, 3030-3632, 3041-3234, 3043-3218, 3094-3380, 3095-3673, 3115-3421, 3122-3762, 3130-3430, 3132-3716, 3145-3404, 3145-3643, 3148-3675, 3155-3720, 3156-3605, 3156-3688, 3156-3734, 3197-3747, 3199-3735, 3202-3810, 3203-3887, 3234-3605, 3239-3605, 3267-3548, 3288-3572, 3289-3574, 3293-3828, 3307-3587, 3323-3796, 3328-3531, 3330-3636, 3344-3607, 3346-3617, 3352-3619, 3355-3808, 3360-3638, 3361-3825, 3363-3553, 3363-3635, 3363-3636, 3374-4035, 3389-4044, 3406-3835, 3408-3725, 3414-4023, 3416-3666, 3422-3682, 3422-3915, 3437-3701, 3453-3740, 3455-3699, 3456-3717, 3456-3720, 3471-3698, 3473-4098, 3478-3736, 3481-3954, 3486-3938,</p> <p>3494-3783, 3495-3752, 3498-3722, 3499-3769, 3512-4105, 3514-4048, 3515-3768, 3522-3795, 3530-4144, 3543-4119, 3549-3882, 3561-4141, 3582-4195, 3589-3812, 3589-4165, 3591-4119, 3591-4211, 3594-4090, 3596-3878, 3601-3877, 3603-3817, 3603-3917, 3608-3885, 3615-4105, 3619-3876, 3627-3774, 3630-4094, 3631-3882, 3631-3979, 3632-3792, 3632-3901, 3634-4105, 3639-3873, 3640-4148, 3640-4208, 3641-4094, 3642-3949, 3644-4081, 3646-3859, 3646-3872, 3648-4097, 3651-3875, 3652-3897, 3652-4103, 3663-4060, 3665-4094, 3671-3939, 3671-3982, 3674-4181, 3677-3956, 3677-4078, 3683-4095, 3686-3930, 3687-4094, 3689-4205, 3691-4211, 3695-4152, 3706-4146, 3708-3958, 3716-3932, 3717-3992, 3717-3993, 3719-4007, 3721-4182, 3723-4186, 3724-3867, 3729-4006, 3732-4186, 3734-4186, 3737-4186, 3738-4035, 3738-4205, 3739-4103, 3739-4204, 3740-4191, 3742-4186, 3743-4056, 3743-4181, 3749-4150, 3751-4204, 3752-4186, 3754-4012, 3754-4186, 3758-4208, 3764-3947, 3764-4182, 3765-4180, 3768-4186, 3770-3955, 3772-4012, 3785-4178, 3788-4049, 3792-4179, 3793-4091, 3799-4204, 3805-4187, 3806-4094, 3825-4181, 3833-4095, 3839-4105, 3841-4103, 3844-4058, 3845-4127,</p> <p>3855-4146, 3859-4185, 3860-4158, 3870-4186, 3880-4179, 3881-4179, 3889-4114, 3904-4148, 3906-4186, 3906-4201, 3953-4186, 3954-4181, 3960-4186, 3960-4187, 3967-4093, 3986-4194, 3995-4186, 4010-4208, 4028-4147, 4028-4186, 4029-4205, 4031-4129, 4033-4181, 4073-4186</p>

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
31/5496710CB1/ 5006	1-240, 1-548, 1-2915, 20-548, 81-709, 81-839, 92-548, 103-322, 162-694, 242-2395, 485-1087, 509-1268, 723-1268, 739-1268, 1050-1087, 1467-1600, 1467-1602, 1515-1921, 1515-1921, 1650-1799, 1703-1993, 2012-2041, 2040-2443, 2066-2323, 2073-2395, 2150-2554, 2151-2462, 2263-2502, 2303-2730, 2368-2633, 2443-2716, 2464-3139, 2490-2861, 2735-2913, 2765-2915, 2920-3172, 2920-3260, 3096-3406, 3153-3589, 3180-3463, 3222-3371, 3297-3520, 3301-3967, 3323-3816, 3426-4028, 3429-3663, 3462-3718, 3462-3887, 3481-3985, 3483-3744, 3694-4131, 3746-4046, 3786-4623, 3802-4134, 3810-4400, 3859-4097, 3890-4112, 3906-4168, 3948-4232, 3973-4532, 3975-4384, 3988-4411, 4001-4601, 4173-4633, 4187-4633, 4190-4633, 4328-4638, 4354-4380, 4354-4384, 4354-4385, 4355-4385, 4359-4562, 4359-4564, 4359-4645, 4375-4589, 4380-4735, 4410-5006, 4414-4633, 4416-4633
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	2829-3458, 2857-3444, 2860-3726, 2876-3491, 2884-3685, 2893-3611, 2894-3473, 2896-3190, 2899-3736, 2906-3516, 2912-3427, 2920-3537, 2923-3614, 2925-3429, 2948-3587, 2953-3672, 2970-3241, 2970-3433, 2983-3561, 2997-3543, 3010-3749, 3022-3673, 3052-3618, 3057-3700, 3057-3707, 3061-3711, 3082-3626, 3083-3780, 3096-3621, 3099-3649, 3114-3773, 3128-3685, 3586-4072, 3586-4072, 3586-4125, 3653-3839, 3653-3864, 3653-3970, 3694-3948, 3731-4125, 3740-3989, 3787-4085, 3844-4125

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
33/6799476CB1/ 3597	1-509, 1-799, 231-856, 259-861, 313-619, 357-851, 378-930, 405-527, 405-694, 405-697, 405-705, 416-711, 432-679, 440-1080, 441-975, 459-819, 472-1164, 503-944, 503-947, 503-1085, 533-806, 538-834, 538-1165, 543-1167, 546-1094, 556-830, 559-1014, 566-1050, 576-775, 579-1167, 583-1058, 584-1165, 588-1165, 596-880, 606-1130, 606-1165, 610-841, 619-808, 619-1228, 626-1013, 626-1111, 626-1114, 629-900, 637-1136, 640-894, 640-1132, 642-768, 649-959, 667-1136, 668-1136, 670-948, 673-903, 673-1113, 673-1136, 676-1136, 676-1151, 679-780, 679-1136, 681-1136, 683-1136, 683-1165, 683-1170, 687-1136, 687-1151, 689-1114, 690-1151, 692-1136, 694-1136, 696-1136, 699-1136, 701-1136, 701-1164, 708-1155, 712-961, 714-1118, 720-1136, 722-1155, 745-1163, 747-1006, 747-1007, 755-1136, 758-1136, 759-1136, 764-1011, 774-1136, 817-1375, 827-1136, 827-1552, 830-1362, 830-1426, 832-1353, 836-1374, 840-1418, 846-1497, 855-1426, 869-1604, 870-1420, 872-1381, 881-1478, 886-1426, 890-1415, 913-1605, 953-1634, 955-1363, 960-1535, 974-1240, 988-1252, 1013-1621, 1032-1545, 1043-1597, 1053-1222, 1075-1505, 1089-1613, 1156-2039, 1175-1844, 1252-1456, 1255-1684, 1331-1954, 1374-1899, 1374-1901, 1437-2275, 1479-1883, 1738-2015, 1738-2186, 1749-2007, 1760-2050, 1768-1968, 1783-1982, 1818-2059, 1818-2387, 1929-2190, 1947-2249, 1995-2255, 2002-2244, 2002-2407, 2018-2232, 2041-2291, 2096-2298, 2096-2321, 2096-2506, 2125-2337, 2125-2384, 2142-2359, 2145-2447, 2149-2325, 2152-2388, 2169-2429, 2195-2452, 2212-2452, 2291-2506, 2291-2763, 2352-2615, 2352-2886, 2368-2432, 2374-2982, 2377-3055, 2378-3198, 2379-2625, 2391-3198, 2423-2977, 2430-3077, 2434-3016, 2437-2667, 2458-3009, 2512-2982, 2519-3098, 2531-3005, 2542-2763, 2542-2979, 2543-3032, 2547-3271, 2555-3222, 2557-3045, 2562-3175, 2564-2790, 2567-3142, 2578-3011, 2584-3043, 2584-3187, 2594-3218, 2605-3198, 2613-3208, 2626-3208, 2627-3330, 2635-2924, 2638-2878, 2644-2980, 2649-3323, 2656-3108, 2669-3208, 2677-2927, 2682-3004, 2682-3225, 2684-3205, 2687-3328, 2692-2893, 2692-3114, 2698-3320, 2712-3120, 2714-2978, 2715-3315, 2719-3193, 2724-2990, 2737-2951, 2760-3398, 2767-3253, 2767-3371, 2770-3010, 2780-3075, 2781-3030, 2782-3144, 2788-3293, 2788-3456, 2790-3245, 2791-3045, 2791-3286, 2793-3533, 2794-3447, 2804-3331, 2805-3046, 2808-2969, 2812-3025, 2813-3383, 2823-3460, 2830-3048, 2831-3400, 2832-3400, 2834-3137, 2849-3377, 2849-3446, 2851-3362, 2851-3440, 2854-3473, 2867-3396, 2876-3446, 2879-3178, 2884-3505, 2888-3142, 2889-3080, 2889-3447, 2891-3448, 2892-3438, 2894-3012, 2894-3172, 2894-3444, 2894-3449, 2896-3597, 2900-3122, 2902-3192, 2906-3155, 2906-3590, 2909-3163, 2909-3460, 2911-3147, 2911-3153, 2911-3399, 2919-3014, 2919-3117, 2922-3181, 2923-3417, 2924-3165, 2927-3167, 2927-3211, 2932-3160, 2935-3188, 2937-3210, 2944-3183, 2954-3203, 2961-3266

Table 4

Polynucleotide SEQ ID NO:/ Incyte ID/ Sequence Length	Sequence Fragments
34/7509488CB1/ 3569	<p>1-567, 47-622, 221-487, 255-514, 271-723, 271-787, 298-781, 328-796, 355-806, 373-807, 393-481, 393-499, 393-591, 393-666, 393-669, 393-677, 393-683, 393-771, 393-823, 393-828, 393-833, 396-902, 396-902, 396-902, 404-651, 412-1052, 413-947, 431-791, 444-1136, 475-613, 475-916, 475-919, 475-1057, 505-778, 510-806, 510-806, 510-1137, 515-1139, 518-1066, 528-802, 531-986, 538-1022, 548-747, 548-861, 551-1139, 555-1030, 556-1137, 560-1137, 568-852, 578-1102, 578-1137, 582-813, 591-780, 591-1200, 598-985, 598-1083, 598-1086, 601-872, 609-1108, 612-866, 612-1104, 614-740, 615-869, 621-931, 639-1108, 640-1108, 642-920, 645-875, 645-1085, 645-1108, 648-1108, 648-1108, 651-752, 651-1108, 653-1108, 655-1108, 659-1108, 659-1123, 662-1123, 664-1108, 666-1108, 668-1108, 671-1108, 673-1108, 680-1127, 684-933, 686-1090, 692-1108, 694-1127, 719-978, 719-979, 727-1108, 730-1108, 731-1108, 746-1108, 789-1347, 799-1108, 799-1524, 802-1334, 802-1398, 804-1325, 808-1346, 812-1390, 818-1469, 827-1398, 841-1576, 842-1392, 844-1353, 853-1450, 858-1398, 862-1387, 885-1577, 925-1606, 927-1335, 932-1507, 946-1212, 960-1224, 985-1593, 1004-1517, 1015-1569, 1025-1194, 1047-1477, 1061-1585,</p> <p>1128-2011, 1147-1816, 1224-1428, 1227-1656, 1303-1926, 1346-1871, 1346-1873, 1409-2247, 1451-1855, 1710-1987, 1710-2158, 1721-1979, 1732-2022, 1740-1940, 1755-1954, 1790-2031, 1790-2359, 1901-2162, 1919-2221, 1967-2227, 1974-2216, 1974-2379, 1990-2204, 2013-2263, 2068-2270, 2068-2293, 2068-2478, 2097-2309, 2097-2356, 2114-2331, 2117-2419, 2121-2297, 2124-2360, 2141-2401, 2167-2424, 2184-2424, 2263-2478, 2263-2735, 2324-2587, 2324-2858, 2340-2404, 2346-2954, 2349-3027, 2350-3170, 2351-2597, 2363-3170, 2395-2949, 2402-3049, 2406-2988, 2409-2639, 2430-2981, 2484-2954, 2491-3070, 2503-2977, 2514-2735, 2514-2951, 2515-3004, 2519-3243, 2527-3194, 2529-3017, 2534-3147, 2536-2762, 2539-3114, 2550-2983, 2556-3015, 2556-3159, 2566-3190, 2577-3170, 2585-3180, 2598-3180, 2599-3302, 2607-2896, 2610-2850, 2616-2952, 2621-3295, 2628-3080, 2641-3180, 2649-2899, 2654-2976, 2654-3197, 2656-3177, 2659-3300, 2664-2865, 2664-3086, 2670-3292, 2684-3092, 2686-2950, 2687-3287, 2691-3165, 2696-2962, 2709-2923, 2732-3370, 2739-3225, 2739-3343, 2742-2982, 2752-3047, 2753-3002, 2754-3116, 2760-3265, 2760-3428, 2762-3217, 2763-3017, 2763-3258,</p> <p>2765-3505, 2766-3419, 2776-3303, 2777-3018, 2780-2941, 2784-2997, 2785-3355, 2795-3432, 2802-3020, 2803-3372, 2804-3372, 2806-3109, 2821-3349, 2821-3418, 2823-3334, 2823-3412, 2826-3445, 2839-3368, 2848-3108, 2848-3418, 2851-3150, 2856-3477, 2859-3106, 2860-3114, 2861-3052, 2861-3419, 2863-3420, 2864-3410, 2866-2984, 2866-3144, 2866-3416, 2866-3421, 2868-3569, 2872-3094, 2874-3164, 2878-3127, 2878-3562, 2881-3135, 2881-3432, 2883-3119, 2883-3125, 2883-3371, 2891-2986, 2891-3089, 2894-3153, 2895-3389, 2896-3137, 2899-3139, 2899-3183, 2904-3132, 2907-3160, 2909-3182, 2916-3155, 2926-3175, 2933-3238</p>

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
35/7510060CB1/ 2431	1-530, 12-268, 12-640, 14-251, 14-566, 14-579, 14-632, 14-653, 14-686, 14-697, 17-572, 25-343, 26-579, 26-657, 26-672, 26-693, 26-716, 27-296, 27-437, 27-685, 27-876, 27-2426, 30-320, 31-234, 33-339, 34-551, 37-599, 39-635, 41-275, 42-352, 43-587, 43-714, 43-726, 43-801, 43-840, 43-853, 43-854, 43-857, 43-867, 44-561, 47-721, 48-302, 50-479, 239-890, 381-983, 414-997, 421-680, 421-692, 465-569, 520-1196, 566-839, 569-832, 569-1146, 574-1221, 591-1202, 712-1329, 733-1049, 733-1118, 786-1062, 800-1011, 832-1373, 856-1117, 885-1400, 889-1465, 928-1148, 973-1473, 1078-1371, 1120-1477, 1152-1352, 1153-1644, 1159-1426, 1165-1760, 1168-1789, 1192-1476, 1193-1473, 1197-1657, 1210-1512, 1233-1480, 1248-1568, 1261-1506, 1331-1582, 1397-1516, 1399-1953, 1406-1696, 1409-1700, 1416-1645, 1416-1664, 1428-2344, 1438-1681, 1455-1711, 1477-1553, 1480-1707, 1523-1781, 1544-2344, 1572-2344, 1737-1990, 1737-1991, 1760-2424, 1762-1827, 1796-2286, 1843-2357, 1950-2351, 1950-2393, 1954-2403, 1965-2376, 2000-2431, 2013-2426, 2059-2309, 2087-2415, 2098-2415, 2099-2417, 2100-2412, 2110-2412, 2112-2413, 2177-2427, 2216-2415, 2227-2415, 2238-2415, 2287-2426, 2299-2406, 2299-2426
36/7510226CB1/ 3842	1-442, 1-3737, 802-1028, 869-1196, 1090-1337, 1117-1318, 1473-2148, 1478-2258, 1478-2284, 1481-2279, 1549-2159, 1556-1777, 1631-2169, 1632-2077, 1632-2166, 1641-2091, 1643-2347, 1648-2086, 1649-2268, 1653-2236, 1663-2374, 1664-2442, 1679-2167, 1706-2185, 1727-2327, 1734-2437, 1735-2148, 1738-2281, 1756-2330, 1756-2333, 1757-2284, 1762-2409, 1762-2488, 1781-2405, 1791-2563, 1792-2215, 1793-2054, 1793-2083, 1802-2112, 1804-2276, 1808-2200, 1809-2312, 1825-2504, 1825-2704, 1827-2362, 1833-2522, 1839-2125, 1856-2484, 1863-2541, 1872-2394, 1885-2064, 1885-2224, 1936-2513, 1939-2220, 1951-2213, 1952-2608, 1957-2220, 1963-2700, 1977-2548, 1980-2238, 1980-2450, 1989-2483, 2002-2703, 2026-2426, 2026-2738, 2029-2615, 2050-2813, 2066-2783, 2070-2767, 2072-2312, 2107-2727, 2108-2419, 2109-2616, 2119-2338, 2122-2360, 2134-2394, 2142-2689, 2146-2829, 2147-2801, 2159-2322, 2167-2286, 2176-2415, 2179-2542, 2182-2445, 2193-2887, 2214-2815, 2216-2782, 2218-2468, 2219-2455, 2231-2866, 2245-2555, 2270-2567, 2275-2968, 2293-2520, 2294-2499,

Table 4

Polynucleotide SEQ ID NO:/ Incyte ID/ Sequence Length	Sequence Fragments
36 cont	<p>2294-2892, 2297-2520, 2306-2459, 2311-2583, 2312-2857, 2317-2882, 2331-2899, 2354-2772, 2355-2583, 2359-2581, 2375-2588, 2378-3008, 2386-2586, 2395-2637, 2410-2673, 2410-2681, 2412-2960, 2416-2939, 2417-2945, 2417-3010, 2420-3096, 2423-2716, 2423-2962, 2444-2711, 2445-3193, 2464-2888, 2471-2706, 2481-2759, 2490-2734, 2494-2753, 2494-2758, 2494-3154, 2497-3112, 2500-2741, 2501-2799, 2508-2963, 2509-2790, 2510-2760, 2510-2818, 2511-2701, 2512-3112, 2531-3112, 2533-3083, 2537-2959, 2548-3033, 2552-2827, 2552-3194, 2571-2835, 2572-3197, 2577-3201, 2591-2837, 2593-2814, 2598-2875, 2607-3112, 2608-3112, 2616-3041, 2619-2872, 2619-2892, 2620-2917, 2622-2906, 2627-3524, 2636-2903, 2642-2793, 2645-2746, 2645-2929, 2655-3112, 2658-3179, 2658-3290, 2661-3175, 2682-3229, 2684-3171, 2686-2969, 2693-2903, 2695-3170, 2698-2964, 2698-3112, 2700-2958, 2700-3170, 2700-3178, 2711-2973, 2711-3175, 2717-2953, 2718-3420, 2722-3314, 2730-2986, 2733-2947, 2735-3183, 2737-3241, 2738-3104, 2744-3195, 2762-3223, 2763-3414, 2765-3223,</p> <p>2770-3059, 2770-3319, 2771-3054, 2771-3480, 2775-3460, 2779-3050, 2789-3049, 2837-2901, 2867-3137, 2868-3196, 2870-3655, 2877-3150, 2880-3136, 2880-3279, 2884-3173, 2886-3158, 2886-3167, 2895-2983, 2895-3143, 2897-3191, 2900-3507, 2910-3463, 2917-3398, 2934-3294, 2935-3198, 2943-3647, 2947-3008, 2948-3177, 2950-3153, 2951-3212, 2962-3217, 2962-3279, 2963-3472, 2963-3695, 2969-3246, 2969-3630, 2971-3250, 2971-3287, 2971-3514, 2972-3410, 2972-3636, 2976-3554, 2980-3571, 2990-3248, 2997-3275, 2997-3283, 3000-3655, 3003-3467, 3004-3228, 3008-3625, 3011-3468, 3012-3290, 3013-3273, 3015-3446, 3018-3274, 3020-3410, 3028-3572, 3029-3523, 3030-3424, 3033-3300, 3034-3251, 3042-3295, 3048-3608, 3051-3488, 3051-3653, 3052-3652, 3053-3488, 3057-3644, 3058-3660, 3062-3632, 3064-3269, 3071-3309, 3071-3433, 3071-3486, 3072-3449, 3073-3663, 3075-3374, 3077-3196, 3077-3548, 3085-3472, 3086-3568, 3098-3719, 3100-3415, 3100-3533, 3103-3709, 3105-3659, 3108-3361, 3108-3392, 3108-3572, 3112-3704, 3118-3392, 3121-3519, 3124-3721, 3129-3285,</p>

Table 4

Polynucleotide SEQ ID NO:/ Incyte ID/ Sequence Length	Sequence Fragments
36 cont	3132-3598, 3138-3319, 3153-3726, 3157-3415, 3157-3447, 3157-3449, 3161-3300, 3161-3375, 3161-3410, 3163-3404, 3163-3441, 3163-3700, 3166-3634, 3166-3653, 3169-3728, 3171-3346, 3171-3420, 3171-3443, 3171-3454, 3172-3687, 3175-3455, 3183-3383, 3184-3657, 3184-3715, 3185-3449, 3185-3725, 3185-3727, 3190-3664, 3190-3730, 3199-3454, 3207-3440, 3207-3457, 3208-3702, 3208-3703, 3211-3708, 3212-3457, 3214-3458, 3214-3724, 3226-3664, 3234-3517, 3236-3699, 3238-3478, 3241-3703, 3247-3703, 3248-3414, 3248-3485, 3248-3706, 3250-3666, 3256-3710, 3257-3673, 3258-3642, 3258-3674, 3265-3585, 3265-3728, 3270-3721, 3270-3724, 3272-3708, 3272-3731, 3273-3702, 3273-3704, 3273-3725, 3273-3737, 3274-3701, 3275-3679, 3275-3710, 3276-3703, 3277-3706, 3279-3704, 3279-3758, 3286-3563, 3287-3725, 3293-3567, 3295-3721, 3295-3731, 3297-3511, 3305-3711, 3306-3542, 3306-3638, 3307-3705, 3309-3702, 3310-3702, 3315-3699, 3315-3703, 3317-3710, 3319-3605, 3320-3704, 3321-3723, 3323-3709, 3324-3579, 3324-3703, 3325-3668, 3330-3706, 3332-3709, 3333-3703, 3334-3705, 3337-3703, 3342-3701, 3345-3626, 3346-3664, 3348-3707, 3351-3549, 3352-3439, 3362-3703, 3384-3703, 3392-3555, 3394-3555, 3406-3709, 3413-3705, 3414-3716, 3415-3512, 3415-3777, 3415-3842, 3420-3769, 3420-3774, 3427-3678, 3427-3687, 3431-3658, 3441-3695, 3447-3703, 3451-3705, 3452-3725, 3455-3703, 3458-3730, 3462-3700, 3464-3703, 3466-3709, 3486-3704, 3491-3749, 3492-3717, 3494-3718, 3514-3702, 3524-3717, 3527-3682, 3534-3753, 3536-3703, 3541-3703, 3547-3698, 3570-3711, 3605-3737, 3605-3739, 3612-3731, 3614-3703, 3638-3708, 3650-3703, 3652-3703 1-113, 1-114, 1-247, 1-260, 6-287, 6-2883, 9-292, 12-309, 14-288, 22-332, 26-624, 38-623, 66-771, 67-513, 71-686, 77-487, 84-771, 97-602, 99-644, 125-624, 126-693, 146-577, 148-734, 168-769, 180-759, 181-759, 194-446, 194-455, 211-951, 213-951, 218-478, 235-784, 275-771, 283-771, 287-698, 319-883, 319-960, 345-771, 354-771, 366-469, 403-602, 515-767, 518-1053, 525-767, 552-892, 638-1135, 670-975, 675-944, 677-933, 726-1311, 741-1311, 850-1513, 1027-1273, 1029-1453, 1098-1631, 1127-1363, 1235-1649, 1240-1681, 1258-1405, 1277-1920, 1278-1704, 1288-1848, 1295-1383, 1319-1593, 1330-1634, 1335-1885, 1362-1667, 1380-1625, 1439-1648, 1454-1716, 1454-1731, 1474-1604, 1479-1845, 1496-2043, 1497-1688, 1513-1736, 1518-1709, 1519-1757, 1529-1769, 1529-1805, 1536-1665, 1546-1919, 1551-1859, 1559-1859, 1568-1824, 1574-1847, 1637-2222, 1640-1943, 1651-1975, 1651-1980, 1668-1947, 1674-2288, 1682-1849, 1693-2020, 1693-2495, 1756-1969, 1769-2253, 1779-2283, 1799-2022, 1799-2547, 1831-2354, 1835-2555, 1836-1969, 1840-2223, 1843-2078, 1843-2079, 1854-2115, 1884-2149, 1917-2582, 1919-2197, 1921-2028, 1921-2191, 1921-2289, 1931-2670, 1934-2209, 1943-2371,
37/7510385CB1/ 2892	

Table 4

Polynucleotide SEQ ID NO:/ Incyte ID/ Sequence Length	Sequence Fragments
37 cont	<p>1944-2675, 1945-2433, 1950-2387, 1950-2451, 1983-2619, 1995-2175, 2004-2786, 2004-2816, 2026-2475, 2034-2286, 2043-2530, 2076-2818, 2086-2693, 2089-2878, 2097-2437, 2129-2322, 2129-2404, 2138-2693, 2138-2807, 2140-2803, 2141-2694, 2145-2543, 2159-2481, 2160-2808, 2162-2317, 2168-2708, 2175-2433, 2178-2399, 2182-2864, 2185-2390, 2220-2361, 2222-2361, 2229-2860, 2245-2494, 2246-2556, 2265-2564, 2265-2616, 2269-2883, 2282-2552, 2301-2548, 2301-2589, 2303-2558, 2303-2571, 2325-2883, 2328-2843, 2330-2883, 2335-2883, 2338-2767, 2342-2590, 2348-2606, 2352-2580, 2352-2797, 2353-2545, 2354-2552, 2355-2570, 2359-2611, 2367-2841, 2371-2800, 2396-2856, 2397-2837, 2408-2513, 2409-2892, 2410-2651, 2427-2883, 2432-2880, 2435-2883, 2438-2883, 2446-2860, 2453-2887, 2460-2613, 2460-2860, 2466-2754, 2467-2879, 2468-2892, 2469-2887, 2470-2860, 2475-2696, 2475-2702, 2477-2843, 2477-2883, 2479-2860, 2483-2879, 2484-2879, 2486-2892, 2493-2857, 2500-2860, 2504-2757, 2507-2859, 2508-2857, 2509-2858, 2512-2880, 2515-2860, 2527-2780, 2529-2804, 2529-2809, 2532-2785, 2545-2823, 2548-2879, 2551-2790, 2555-2787, 2570-2888, 2577-2883,</p> <p>2580-2857, 2581-2883, 2584-2886, 2586-2892, 2587-2871, 2590-2857, 2600-2879, 2606-2843, 2606-2860, 2616-2829, 2629-2863, 2633-2874, 2647-2837, 2648-2821, 2649-2857, 2657-2881, 2661-2883, 2664-2853, 2664-2855, 2664-2856, 2664-2870, 2664-2872, 2664-2885, 2666-2879, 2668-2870, 2669-2879, 2670-2856, 2670-2870, 2670-2877, 2670-2879, 2675-2883, 2676-2892, 2677-2860, 2678-2883, 2693-2857, 2698-2883, 2703-2892, 2740-2786, 2743-2879, 2759-2883, 2771-2872, 2771-2883</p>
38/7511618CB1/ 2756	<p>1-424, 1-2756, 46-423, 57-295, 57-310, 57-412, 57-413, 62-415, 98-235, 104-406, 107-424, 132-402, 136-424, 417-518, 417-839, 519-754, 519-765, 519-773, 519-782, 519-783, 519-844, 519-996, 519-1103, 521-972, 541-983, 541-1138, 571-1058, 586-1252, 589-970, 598-948, 598-953, 614-1058, 626-1102, 635-1138, 645-913, 654-1124, 666-1249, 667-1021, 668-926, 668-1031, 674-933, 675-924, 691-1319, 696-953, 718-1188, 727-997, 732-1058, 733-1132, 743-1124, 748-1049, 753-1324, 792-1025, 796-1193, 801-1087, 805-1123, 807-1193, 819-1224, 846-1137, 881-1058, 901-1184, 903-1777, 920-1192, 931-1213, 933-1644, 972-1265, 972-1566, 998-1593, 1008-1275, 1021-1187, 1038-1319, 1046-1491, 1046-1546, 1061-1296, 1083-1335, 1108-1626, 1136-1160, 1136-1281, 1136-1302, 1136-1529, 1137-1581, 1157-1536, 1158-1708, 1182-1434, 1183-1871, 1191-1454, 1195-1717, 1197-1692, 1218-1495, 1218-1609, 1251-1522, 1267-1907, 1272-1563, 1281-1505, 1286-1561, 1323-1654, 1331-1556, 1331-1767, 1350-1592, 1356-1592, 1374-1694, 1377-1898, 1400-1655, 1417-1725, 1425-1653, 1425-1668, 1427-1594, 1433-1818, 1440-1954, 1442-1929, 1459-1741, 1477-1623, 1478-1745, 1483-1939, 1490-1651, 1493-1955,</p>

Table 4

Polynucleotide SEQ ID NO./ Incye ID/ Sequence Length	Sequence Fragments
38 cont	1505-1927, 1509-2147, 1510-1954, 1513-1931, 1516-1954, 1519-1806, 1527-1937, 1532-2047, 1534-2068, 1537-2121, 1540-1822, 1543-1953, 1549-1936, 1560-1954, 1564-1954, 1573-1846, 1586-1954, 1596-1937, 1596-1947, 1610-1950, 1616-1794, 1625-1920, 1628-1940, 1629-1922, 1645-1881, 1645-2131, 1646-1886, 1646-1930, 1646-2155, 1667-1928, 1670-1950, 1678-1957, 1693-1953, 1712-1990, 1713-1989, 1723-1935, 1729-1908, 1738-2122, 1746-2414, 1788-2081, 1820-2178, 1820-2297, 1823-1935, 1828-2101, 1828-2298, 1846-2103, 1851-2365, 1870-2148, 1889-2500, 1908-2445, 1920-2492, 1943-2239, 1945-2100, 1957-2193, 1957-2194, 1969-2392, 1969-2436, 1971-2243, 1973-2232, 1987-2274, 1994-2486, 1995-2299, 2014-2299, 2034-2477, 2044-2492, 2047-2477, 2054-2342, 2058-2471, 2060-2278, 2060-2631, 2062-2471, 2068-2485, 2068-2489, 2071-2346, 2072-2335, 2076-2472, 2087-2486, 2090-2666, 2106-2367, 2110-2317, 2110-2450, 2114-2626, 2115-2201, 2122-2684, 2123-2490, 2126-2487, 2149-2669, 2149-2676, 2156-2543, 2162-2457, 2168-2541, 2187-2466, 2187-2626, 2208-2541, 2215-2631, 2226-2487, 2228-2459, 2236-2504, 2307-2680, 2334-2587, 2340-2746,
	2343-2547, 2348-2492, 2348-2614, 2399-2624, 2443-2681, 2475-2756, 2495-2678, 2558-2680
39/6244135CB1/ 873	1-302, 12-348, 14-302, 106-836, 124-413, 165-714, 165-727, 165-771, 206-477, 326-506, 392-639, 447-705, 459-873, 497-827, 499-683, 607-873
40/7506689CB1/ 2660	1-218, 1-411, 1-811, 36-718, 115-408, 148-405, 151-399, 265-408, 407-538, 407-577, 407-611, 407-617, 407-650, 407-675, 407-740, 407-750, 407-787, 407-804, 407-957, 407-2595, 408-1113, 489-1018, 515-1111, 515-1112, 538-813, 558-1111, 572-1067, 577-1089, 581-1108, 602-1111, 603-675, 605-1111, 606-1111, 609-1111, 613-923, 613-1111, 618-1111, 620-956, 620-1083, 620-1166, 620-1236, 624-1111, 671-1111, 674-1111, 715-934, 715-955, 715-1159, 715-1218, 715-1228, 715-1253, 715-1284, 719-1313, 757-1111, 881-1397, 888-1318, 899-1455, 941-1075, 973-1480, 1055-1418, 1086-1632, 1094-1381, 1100-1686, 1148-1702, 1186-1656, 1190-1437, 1196-1429, 1196-1758, 1204-1313, 1222-1749, 1225-1797, 1251-1590, 1349-1748, 1349-1979, 1418-1943, 1420-1954, 1422-1943, 1436-2352, 1456-1925, 1473-2011, 1485-2111, 1491-2352, 1499-2352, 1520-2032, 1532-2352, 1536-1810, 1592-2352, 1612-2191, 1615-2348, 1632-2216, 1635-2125, 1659-2352, 1669-2190, 1677-2352, 1682-2380, 1684-1892, 1700-2352, 1711-2162, 1729-2394, 1738-2353, 1742-2449, 1772-2017, 1776-2398, 1777-2386, 1780-2454, 1784-2203, 1842-2439, 1865-2432, 1909-2454, 1918-2454, 1984-2453, 1986-2454, 1999-2454, 2020-2448,
	2022-2311, 2048-2449, 2051-2660, 2053-2448, 2098-2472, 2135-2450, 2155-2453, 2168-2454, 2207-2438, 2241-2454, 2241-2498, 2386-2454

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
41/7510185CB1/ 2761	1-2759, 103-686, 104-686, 512-784, 512-1040, 685-1492, 796-1296, 1383-1613, 1614-1857, 1614-2035, 1614-2044, 1614-2191, 1614-2240, 1614-2338, 1614-2368, 1614-2374, 1614-2386, 1614-2486, 1678-2262, 1791-2070, 1873-2681, 1888-2165, 1888-2168, 1888-2269, 1888-2344, 1888-2441, 1987-2761, 2026-2524, 2050-2314, 2133-2761, 2195-2761, 2212-2761, 2216-2740, 2242-2457, 2251-2761, 2314-2749, 2315-2745, 2315-2749, 2317-2624, 2317-2656, 2317-2705, 2346-2755, 2371-2761, 2414-2749, 2490-2755
42/1420867CB1/ 1440	1-252, 1-268, 1-311, 1-418, 1-460, 1-511, 1-529, 1-589, 1-605, 1-691, 1-711, 1-732, 1-734, 1-881, 12-814, 44-997, 196-432, 456-1097, 458-896, 458-932, 524-1128, 526-1338, 544-1061, 609-1440, 649-1440, 662-1115, 679-1440, 767-1104, 772-1258, 778-1399, 859-1440, 886-1440, 893-1111, 896-1438, 907-1412, 912-1440, 935-1393, 1005-1440, 1022-1432, 1041-1440, 1068-1326
43/7512289CB1/ 1066	1-205, 20-162, 20-276, 21-255, 30-457, 31-326, 32-323, 32-507, 33-315, 34-277, 34-314, 35-285, 36-130, 36-269, 36-271, 36-275, 36-280, 36-283, 36-289, 36-308, 36-312, 36-319, 36-322, 36-323, 36-331, 36-628, 36-637, 36-654, 38-323, 39-336, 39-654, 40-275, 40-285, 40-303, 40-315, 40-609, 41-304, 41-552, 43-352, 43-619, 44-336, 45-279, 45-512, 46-266, 47-300, 48-199, 48-566, 48-628, 49-342, 49-349, 50-261, 55-298, 55-335, 56-1058, 57-633, 58-299, 58-332, 59-260, 59-300, 59-602, 62-321, 62-648, 63-311, 63-314, 63-340, 63-364, 63-382, 63-462, 63-582, 63-657, 64-243, 64-322, 64-331, 64-659, 65-281, 65-284, 65-300, 65-309, 65-326, 65-338, 65-340, 65-345, 65-349, 65-355, 65-358, 65-372, 65-548, 65-589, 65-616, 65-659, 66-291, 66-309, 66-310, 66-327, 66-334, 66-343, 66-439, 66-659, 67-180, 67-271, 67-341, 67-342, 67-359, 67-373, 67-659, 68-155, 68-370, 69-369, 69-373, 70-301, 70-313, 70-319, 70-320, 70-337, 70-351, 70-359, 70-368, 70-573, 71-276, 71-303, 71-313, 71-422, 72-321, 72-345, 72-349, 72-580, 72-584, 73-269, 73-306, 73-314, 73-358, 73-444, 74-659, 75-321, 75-466, 76-273, 76-351, 76-362, 76-604, 77-234, 77-266, 77-275, 77-281, 77-287, 77-319, 77-320, 77-321, 77-322, 77-331, 77-349, 77-359, 77-362,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
43 cont	77-367, 77-377, 77-387, 78-301, 78-317, 79-347, 79-362, 79-390, 80-186, 80-195, 80-280, 80-314, 80-320, 80-330, 80-335, 80-352, 80-361, 81-332, 81-345, 82-270, 82-314, 82-328, 82-329, 82-337, 82-344, 82-348, 82-351, 82-357, 82-367, 82-380, 82-448, 82-659, 83-483, 83-543, 83-630, 84-358, 87-335, 87-359, 88-287, 88-457, 89-307, 89-320, 89-373, 89-374, 90-365, 91-654, 97-344, 97-550, 99-623, 99-660, 99-685, 101-329, 101-394, 101-548, 105-389, 106- 379, 106-628, 108-426, 111-378, 112-550, 116-415, 118-558, 125-330, 133-381, 133-413, 133-416, 133-435, 138- 371, 139-322, 139-354, 143-379, 150-453, 151-390, 151-410, 157-402, 160-372, 160-659, 169-451, 172-506, 175- 429, 176-434, 176-451, 180-445, 182-448, 185-464, 186-645, 188-342, 189-524, 190-354, 192-464, 193-322, 193- 407, 193-471, 194-345, 194-447, 194-465, 194-502, 195-466, 196-415, 196-419, 196-439, 198-309, 198-423, 198- 438, 198-444, 198-453, 198-659, 199-443, 199-444, 199-447, 199-448, 199-460, 199-472, 199-477, 200-479, 201- 486, 201-573, 203-606, 205-427, 205-436, 205-452, 205-461, 205-462, 205-468, 206-574, 206-606, 208-624, 210- 450, 214-457, 220-614, 221-468, 223-513, 233-604, 236-479, 236-505, 236-507, 236-544, 237-518, 239-483, 240-502, 240-521, 242-385, 242-436, 242-482, 243-377, 243-470, 245-516, 247-520, 248-486, 250-508, 253-588, 254-361, 254-501, 254-515, 254-570, 256-524, 257-501, 257-512, 259-477, 260-540, 260-555, 260-571, 265-521, 265-534, 265-538, 266-450, 267-551, 271-504, 271-520, 271-529, 271-539, 271-600, 274-530, 275-488, 275-533, 277-609, 281-503, 281-541, 281-563, 281-568, 281-572, 283-511, 285-490, 285-553, 285-558, 286-525, 286-562, 291-545, 298-646, 298-657, 300-595, 302-551, 306-536, 306-610, 307-555, 309-568, 309-594, 309-654, 310-614, 312-508, 312-565, 322-508, 322-567, 322-582, 324-496, 326-543, 326-604, 327-556, 329-561, 329-576, 330-563, 330-570, 331-527, 335-584, 336-554, 336-556, 336-558, 336-582, 338-597, 341-659, 342-647, 343-602, 344-616, 344-638, 345-428, 345-540, 345-589, 345-607, 345-616, 346-644, 348-549, 348-570, 348-589, 348-618, 348-627, 350-537, 350-569, 350-582, 351-619, 351-639, 355-625, 357-563, 357-616, 358-596, 360-622, 361-630, 362-508, 362-509, 362-653, 362-659, 365-630, 366-659, 367-533, 367-592, 367-617, 367-618, 370-534, 370-659, 377-611, 377-659, 379-549, 379-649, 380-640, 382-502, 387-557, 388-619, 388-646, 388-659, 389-503,

Table 4

Polynucleotide SEQ ID NO./ Incyte ID/ Sequence Length	Sequence Fragments
43 cont	389-561, 389-630, 389-639, 389-659, 390-613, 391-616, 391-659, 397-656, 398-632, 402-659, 406-624, 406-627, 406-659, 408-580, 408-645, 408-650, 408-659, 411-638, 412-652, 413-638, 414-631, 414-642, 415-647, 417-599, 417-659, 420-659, 421-659, 422-660, 423-582, 423-641, 423-659, 426-659, 428-659, 429-659, 434-654, 439-659, 447-659, 448-659, 456-659, 459-650, 459-659, 460-659, 464-652, 467-630, 470-657, 471-659, 472-659, 475-659, 476-623, 482-648, 486-784, 498-598, 514-659, 521-623, 521-659, 531-659, 544-659, 563-648, 585-659, 668-909, 698-962, 742-946, 754-1000, 823-1064, 880-1066, 925-1063, 927-1060, 936-1056, 946-1060, 972-1066, 973-1060, 986-1060, 987-1060
44/7512447CB1/ 4179	1-162, 52-318, 81-584, 81-612, 84-4056, 103-606, 104-532, 141-612, 141-747, 141-916, 141-932, 142-612, 395-634, 928-1182, 931-1043, 931-1189, 977-1604, 978-1604, 1508-2021, 1581-2075, 1581-2077, 1598-2074, 1721-2310, 1984-2325, 2018-2425, 2018-2614, 2023-2852, 2054-2691, 2085-2723, 2108-2580, 2144-2733, 2146-2407, 2146-2418, 2146-2477, 2163-2350, 2163-2384, 2163-2465, 2232-2935, 2234-2639, 2533-2812, 2586-2843, 2704-3149, 2829-3128, 2829-3141, 2948-3459, 2948-3509, 2953-3610, 2958-3353, 2970-3763, 3033-3264, 3033-3310, 3050-3315, 3086-3411, 3105-3706, 3119-3378, 3291-3828, 3318-4056, 3320-3590, 3376-3752, 3462-3963, 3462-4106, 3488-4179, 3515-3952, 3515-4017, 3515-4042, 3515-4065, 3697-3959, 3702-3942, 3702-3959, 3771-3896, 3773-3959, 3800-3959

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID:	Representative Library
23	7506758CB1	PGANNOT01
24	4381669CB1	BRAXTDR12
25	7503554CB1	TLYMNOT03
26	7506077CB1	OVARNOT03
27	7506765CB1	SCORNON02
28	7490048CB1	BRAIFEC01
29	2133585CB1	ENDCNOT01
30	7509063CB1	PANCTUT02
31	5496710CB1	BRAUNOR01
32	72150826CB1	COLNTUT06
33	6799476CB1	FIBRTXS07
34	7509488CB1	BRANDIT04
35	7510060CB1	CORPNOT02
36	7510226CB1	KIDEUNE02
37	7510385CB1	SINTNOR01
38	75111618CB1	ADRETUE04
39	6244135CB1	TESTNOT17
40	7506689CB1	PLACFER01
41	7510185CB1	LNOMNOF03
42	1420867CB1	BLADTUT03
43	7512289CB1	MPHGNOT03
44	7512447CB1	SINTNOR01

Table 6

Library	Vector	Library Description
ADRETUE04	PCDNA2.1	This 5 prime biased random primed library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma. Patient history included benign hypertension, depressive disorder, chronic sinusitis, idiopathic proctocolitis, a cataract, and urinary tract infection. Previous surgeries included a vaginal hysterectomy. Patient medications included Procardia (one dose only) and Prozac for 5 years. Family history included secondary Parkinsonism in the father; cerebrovascular disease, secondary Parkinsonism and anxiety state in the mother; and benign hypertension, atherosclerotic coronary artery disease, hyperlipidemia, and brain cancer in the sibling(s).
BLADTUT03	pINCY	Library was constructed using RNA isolated from bladder tumor tissue removed from a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, regional lymph node excision, and urinary diversion to bowel. Pathology indicated invasive grade 3 transitional cell carcinoma. Patient history included a benign colon neoplasm. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
BRAIFEC01	pINCY	This large size-fractionated library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus who was stillborn with a hypoplastic left heart at 23 weeks' gestation.
BRANDJT04	pINCY	Library was constructed using RNA isolated from pineal gland tissue removed from a 68-year-old Caucasian female who died from congestive heart failure. Neuropathology indicated mild to moderate Alzheimer disease, atherosclerosis, and multiple infarctions. Microscopically, there were diffuse and neuritic amyloid plaques throughout the cerebral cortex. There were neurofibrillary tangles in the temporal lobes particularly the entorhinal cortex. The frontal cortex contained scattered, ballooned neurons. The amygdala contained marked gliosis, neuritic plaques and intracellular neurofibrillary tangles. The hippocampus contained neuritic and diffuse plaques, and neurofibrillary tangles. The thalamus contained diffuse and focal neuritic amyloid plaques and scattered neurofibrillary tangles. There was area of cystic cavitation with surrounding gliosis in the left globus pallidus. The pallidum contained scattered intracellular neurofibrillary tangles.
		The caudate, putamen and nucleus accumbens contained diffuse plaques. There was an area of cystic cavitation with lipid-laden macrophages in the right cerebellar hemisphere. Patient history included diabetes mellitus, rheumatoid arthritis, hyperthyroidism, amyloid heart disease, and dementia.

Table 6

Library	Vector	Library Description
BRAUNOR01	pINCY	This random primed library was constructed using RNA isolated from striatum, globus pallidus and posterior putamen tissue removed from an 81-year-old Caucasian female who died from a hemorrhage and ruptured thoracic aorta due to atherosclerosis. Pathology indicated moderate atherosclerosis involving the internal carotids, bilaterally; microscopic infarcts of the frontal cortex and hippocampus, and scattered diffuse amyloid plaques and neurofibrillary tangles, consistent with age. Grossly, the leptomeninges showed only mild thickening and hyalinization along the superior sagittal sinus. The remainder of the leptomeninges was thin and contained some congested blood vessels. Mild atrophy was found mostly in the frontal poles and lobes, and temporal lobes, bilaterally. Microscopically, there were pairs of Alzheimer type II astrocytes within the
		deep layers of the neocortex. There was increased satellitosis around neurons in the deep gray matter in the middle frontal cortex. The amygdala contained rare diffuse plaques and neurofibrillary tangles. The posterior hippocampus contained a microscopic area of cystic cavitation with hemosiderin-laden macrophages surrounded by reactive gliosis. Patient history included sepsis, cholangitis, post-operative atelectasis, pneumonia CAD, cardiomegaly due to left ventricular hypertrophy, splenomegaly, arteriolonephrosclerosis, nodular colloidal goiter, emphysema, CHF, hypothyroidism, and peripheral vascular disease.
BRAXTDR12	PCDNA2.1	This random primed library was constructed using RNA isolated from frontal neocortex tissue removed from a 55-year-old Caucasian female who died from cholangiocarcinoma. Pathology indicated mild meningeal fibrosis predominately over the convexities, scattered axonal spheroids in the white matter of the cingulate cortex and the thalamus, and a few scattered neurofibrillary tangles in the entorhinal cortex and the periaqueductal gray region. Pathology for the associated tumor tissue indicated well-differentiated cholangiocarcinoma of the liver with residual or relapsed tumor. Patient history included cholangiocarcinoma, post-operative Budd-Chiari syndrome, biliary ascites, hydrothorax, dehydration, malnutrition, oliguria and acute renal failure. Previous surgeries included cholecystectomy and resection of 85% of the liver.
COLNTUT06	pINCY	Library was constructed using RNA isolated from colon tumor tissue obtained from a 45-year-old Caucasian female during a total colectomy and total abdominal hysterectomy. Pathology indicated invasive grade 2 colonic adenocarcinoma forming a cecal mass. Patient history included benign neoplasms of the rectum and anus, multiple sclerosis and mitral valve disorder. Previous surgeries included a polypectomy. Family history included type I diabetes, cerebrovascular disease, atherosclerotic coronary artery disease, malignant skin neoplasm, hypertension, atherosclerotic coronary artery disease and malignant neoplasm of the colon.
CORPNOT02	pINCY	Library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.

Table 6

Library	Vector	Library Description
ENDCNOT01	pINCY	Library was constructed using RNA isolated from endothelial cells removed from the coronary artery of a 58-year-old Hispanic male.
FIBRTXS07	pINCY	This subtracted library was constructed using 1.3 million clones from a dermal fibroblast library and was subjected to two rounds of subtraction hybridization with 2.8 million clones from an untreated dermal fibroblast tissue library. The starting library for subtraction was constructed using RNA isolated from treated dermal fibroblast tissue removed from the breast of a 31-year-old Caucasian female. The cells were treated with 9CIS retinoic acid. The hybridization probe for subtraction was derived from a similarly constructed library from RNA isolated from untreated dermal fibroblast tissue from the same donor. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR (1991) 19:1954 and Bonaldo, et al., Genome Research (1996) 6:791.
KIDEUNE02	pINCY	This 5' biased random primed library was constructed using RNA isolated from an untreated transformed embryonal cell line (293-EBNA) derived from kidney epithelial tissue (Invitrogen). The cells were transformed with adenovirus 5 DNA.
LNOMNOF03	PCMV-ICIS	Library was constructed using RNA isolated from mesenteric lymph node tissue removed from a 13-year-old Caucasian male who died from intracranial bleed. Serologies were negative. Previous surgeries included tonsillectomy.
MPHGNOT03	PBLUESCRIPT	Library was constructed using RNA isolated from plastic adherent mononuclear cells isolated from buffy coat units obtained from unrelated male and female donors.
OVARNOT03	PSPORT1	Library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
PANCTUT02	pINCY	Library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreaticoduodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.
PGANNOT01	PSPORT1	Library was constructed using RNA isolated from paraganglionic tumor tissue removed from the intra-abdominal region of a 46-year-old Caucasian male during exploratory laparotomy. Pathology indicated a benign paraganglioma and was associated with a grade 2 renal cell carcinoma, clear cell type, which did not penetrate the capsule. Surgical margins were negative for tumor.

Table 6

Library	Vector	Library Description
PLACFER01	pINCY	The library was constructed using RNA isolated from placental tissue removed from a Caucasian fetus, who died after 16 weeks' gestation from fetal demise and hydrocephalus. Patient history included umbilical cord wrapped around the head (3 times) and the shoulders (1 time). Serology was positive for anti-CMV. Family history included multiple pregnancies and live births, and an abortion.
SCORNON02	PSPORT1	This normalized spinal cord library was constructed from 3.24M independent clones from the a spinal cord tissue library. RNA was isolated from the spinal cord tissue removed from a 71-year-old Caucasian male who died from respiratory arrest. Patient history included myocardial infarction, gangrene, and end stage renal disease. The normalization and hybridization conditions were adapted from Soares et al.(PNAS (1994) 91:9228).
SINTNOR01	PCDNA2.1	This random primed library was constructed using RNA isolated from small intestine tissue removed from a 31-year-old Caucasian female during Roux-en-Y gastric bypass. Patient history included clinical obesity.
TESTNOT17	pINCY	Library was constructed from testis tissue removed from a 26-year-old Caucasian male who died from head trauma due to a motor vehicle accident. Serologies were negative. Patient history included a hernia at birth, tobacco use (1 1/2 ppd), marijuana use, and daily alcohol use (beer and hard liquor).
TLYMNOT03	pINCY	Library was constructed using RNA isolated from nonactivated Th1 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-12 and B7-transfected COS cells.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value = 1.0E-8 or less; Full Length sequences: Probability value = 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value = 1.06E-6; Assembled ESTs: fasta Identity = 95% or greater and Match length = 200 bases or greater; fastx E value = 1.0E-8 or less; Full Length sequences: fastx score = 100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value = 1.0E-3 or less

Table 7

Program	Description	Reference	Parameter Threshold
HMIMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM, INCY, SMART and TIGRFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM, INCY, SMART or TIGRFAM hits: Probability value = 1.0E-3 or less; Signal peptide hits: Score = 0 or greater
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG specified "HIGH" value for that particular Prosite motif. Generally, score = 1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score = 120 or greater; Match length = 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score = 3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	

Table 7

Program	Description	Reference	Parameter Threshold
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22,
 - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-2, SEQ ID NO:5-6, SEQ ID NO:10, SEQ ID NO:15, and SEQ ID NO:17-19,
 - c) a polypeptide comprising a naturally occurring amino acid sequence at least 95% identical to the amino acid sequence of SEQ ID NO:3,
 - d) a polypeptide comprising a naturally occurring amino acid sequence at least 96% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:9, and SEQ ID NO:14,
 - e) a polypeptide comprising a naturally occurring amino acid sequence at least 97% identical to the amino acid sequence of SEQ ID NO:7,
 - f) a polypeptide comprising a naturally occurring amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of of SEQ ID NO:13, and SEQ ID NO:20,
 - g) a polypeptide consisting essentially of a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:11-12, SEQ ID NO:16, and SEQ ID NO:21-22,
 - h) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and
 - i) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

2. An isolated polypeptide of claim 1 comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

3. An isolated polynucleotide encoding a polypeptide of claim 1.

4. An isolated polynucleotide encoding a polypeptide of claim 2.
5. An isolated polynucleotide of claim 4 comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44.
- 5 6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
7. A cell transformed with a recombinant polynucleotide of claim 6.
- 10 8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
9. A method of producing a polypeptide of claim 1, the method comprising:
- 15 a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and
- b) recovering the polypeptide so expressed.
- 20 10. A method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.
11. An isolated antibody which specifically binds to a polypeptide of claim 1.
- 25 12. An isolated polynucleotide selected from the group consisting of:
- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44,
- b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-28, SEQ ID NO:31-34, SEQ ID NO:36-39, and SEQ ID NO:41,
- 30 c) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 93% identical to the polynucleotide sequence of SEQ ID NO:40,

- d) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 94% identical to the polynucleotide sequence of SEQ ID NO:30,
- e) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 96% identical to the polynucleotide sequence of SEQ ID NO:44,
- 5 f) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 97% identical to the polynucleotide sequence of SEQ ID NO:35,
- g) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 99% identical to the polynucleotide sequence of SEQ ID NO:43,
- h) a polynucleotide consisting essentially of a naturally occurring polynucleotide
10 sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:29, and SEQ ID NO:42
- i) a polynucleotide complementary to a polynucleotide of a),
- j) a polynucleotide complementary to a polynucleotide of b),
- k) a polynucleotide complementary to a polynucleotide of c),
- 15 l) a polynucleotide complementary to a polynucleotide of d),
- m) a polynucleotide complementary to a polynucleotide of e),
- n) a polynucleotide complementary to a polynucleotide of f),
- o) a polynucleotide complementary to a polynucleotide of g),
- p) a polynucleotide complementary to a polynucleotide of h), and
- 20 q) an RNA equivalent of a)-p).

13. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 12.

- 25 14. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:
- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions
30 whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
 - b) detecting the presence or absence of said hybridization complex, and, optionally, if

present, the amount thereof.

15. A method of claim 14, wherein the probe comprises at least 60 contiguous nucleotides.

5 16. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment

10 thereof, and, optionally, if present, the amount thereof.

17. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

15 18. A composition of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

19. A method for treating a disease or condition associated with decreased expression of functional NTRAN, comprising administering to a patient in need of such treatment the composition of

20 claim 17.

20. A method of screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- 25 b) detecting agonist activity in the sample.

21. A composition comprising an agonist compound identified by a method of claim 20 and a pharmaceutically acceptable excipient.

30 22. A method for treating a disease or condition associated with decreased expression of functional NTRAN, comprising administering to a patient in need of such treatment a composition of claim 21.

23. A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

5

24. A composition comprising an antagonist compound identified by a method of claim 23 and a pharmaceutically acceptable excipient.

25. A method for treating a disease or condition associated with overexpression of functional NTRAN, comprising administering to a patient in need of such treatment a composition of claim 24.

26. A method of screening for a compound that specifically binds to the polypeptide of claim 1, the method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and
- b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

15

27. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, the method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

25

30

28. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method

comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- 5 c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

29. A method of assessing toxicity of a test compound, the method comprising:

- a) treating a biological sample containing nucleic acids with the test compound,
- 10 b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 12 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 12 or fragment thereof,
- 15 c) quantifying the amount of hybridization complex, and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

20

30. A method for a diagnostic test for a condition or disease associated with the expression of NTRAN in a biological sample, the method comprising:

- a) combining the biological sample with an antibody of claim 11, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex,
- 25 and
- b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

31. The antibody of claim 11, wherein the antibody is:

- 30 a) a chimeric antibody,
- b) a single chain antibody,
- c) a Fab fragment,
- d) a F(ab')₂ fragment, or

e) a humanized antibody.

32. A composition comprising an antibody of claim 11 and an acceptable excipient.

5 33. A method of diagnosing a condition or disease associated with the expression of NTRAN in a subject, comprising administering to said subject an effective amount of the composition of claim 32.

34. A composition of claim 32, further comprising a label.

10

35. A method of diagnosing a condition or disease associated with the expression of NTRAN in a subject, comprising administering to said subject an effective amount of the composition of claim 34.

15 36. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 11, the method comprising:

- a) immunizing an animal with a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, or an immunogenic fragment thereof, under conditions to elicit an antibody response,
- 20 b) isolating antibodies from the animal, and
- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

25 37. A polyclonal antibody produced by a method of claim 36.

38. A composition comprising the polyclonal antibody of claim 37 and a suitable carrier.

39. A method of making a monoclonal antibody with the specificity of the antibody of claim 30 11, the method comprising:

- a) immunizing an animal with a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, or an immunogenic fragment thereof, under conditions to elicit an antibody response,

- b) isolating antibody producing cells from the animal,
- c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells,
- d) culturing the hybridoma cells, and
- 5 e) isolating from the culture monoclonal antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

10 40. A monoclonal antibody produced by a method of claim 39.

41. A composition comprising the monoclonal antibody of claim 40 and a suitable carrier.

42. The antibody of claim 11, wherein the antibody is produced by screening a Fab expression library.

15 43. The antibody of claim 11, wherein the antibody is produced by screening a recombinant immunoglobulin library.

44. A method of detecting a polypeptide comprising an amino acid sequence selected from
20 the group consisting of SEQ ID NO:1-22 in a sample, the method comprising:
a) incubating the antibody of claim 11 with the sample under conditions to allow specific binding of the antibody and the polypeptide, and
b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide comprising an amino acid sequence selected from the group consisting of
25 SEQ ID NO:1-22 in the sample.

45. A method of purifying a polypeptide comprising an amino acid sequence selected from
the group consisting of SEQ ID NO:1-22 from a sample, the method comprising:
a) incubating the antibody of claim 11 with the sample under conditions to allow specific
30 binding of the antibody and the polypeptide, and
b) separating the antibody from the sample and obtaining the purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

46. A microarray wherein at least one element of the microarray is a polynucleotide of claim 13.

47. A method of generating an expression profile of a sample which contains polynucleotides, the method comprising:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 46 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

48. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, and wherein said target polynucleotide is a polynucleotide of claim 12.

49. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

50. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide.

51. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to said target polynucleotide.

52. An array of claim 48, which is a microarray.

53. An array of claim 48, further comprising said target polynucleotide hybridized to a nucleotide molecule comprising said first oligonucleotide or polynucleotide sequence.

54. An array of claim 48, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

55. An array of claim 48, wherein each distinct physical location on the substrate contains multiple nucleotide molecules, and the multiple nucleotide molecules at any single distinct physical location have the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at
5 another distinct physical location on the substrate.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

10

58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

15

60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

20

63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

25

65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.

30

68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.

69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.

70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.

71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.

5 72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.

73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.

74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.

10

75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.

76. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.

15

77. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.

78. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:23.

79. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:24.

20

80. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:25.

81. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:26.

25

82. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:27.

83. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:28.

84. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:29.

30

85. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:30.

86. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:31.

87. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:32.
88. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:33.
- 5 89. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:34.
90. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:35.
91. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:36.
- 10 92. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:37.
93. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:38.
- 15 94. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:39.
95. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:40.
96. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:41.
- 20 97. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:42.
98. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:43.
- 25 99. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:44.

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YUE, Henry
ZHENG, Wenjin

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Lys Gln Asn Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn		
2150	2155	2160
Ser Ile Trp Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln		
2165	2170	2175
Leu Gln Arg Leu Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu		
2180	2185	2190
Gln Ile Lys Lys Leu Lys Glu Leu Gln Lys Ala Val Asp His Arg		

2195	2200	2205
Lys Ala Ile Ile Leu Ser Ile Asn Leu Cys Ser Pro Glu Phe Thr		
2210	2215	2220
Gln Ala Asp Ser Lys Glu Ser Arg Asp Leu Gln Asp Arg Leu Ser		
2225	2230	2235
Gln Met Asn Gly Arg Trp Asp Arg Val Cys Ser Leu Leu Glu Glu		
2240	2245	2250
Trp Arg Gly Leu Leu Gln Asp Ala Leu Met Gln Cys Gln Gly Phe		
2255	2260	2265
His Glu Met Ser His Gly Leu Leu Leu Met Leu Glu Asn Ile Asp		
2270	2275	2280
Arg Arg Lys Asn Glu Ile Val Pro Ile Asp Ser Asn Leu Asp Ala		
2285	2290	2295
Glu Ile Leu Gln Asp His His Lys Gln Leu Met Gln Ile Lys His		
2300	2305	2310
Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser Leu Gln Asp Met		
2315	2320	2325
Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys Leu Glu		
2330	2335	2340
Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu Leu		
2345	2350	2355
Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu		
2360	2365	2370
Asp Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala		
2375	2380	2385
Asp Glu Leu Asp Thr Ser Gly Ser Val Ser Pro Thr Ser Gly Arg		
2390	2395	2400
Ser Thr Pro Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu		
2405	2410	2415
Ser Gln Pro Gly Pro Ser Val Ser Ser Pro His Ser Arg Ser Thr		
2420	2425	2430
Lys Gly Gly Ser Asp Ser Ser Leu Ser Glu Pro Gly Pro Gly Arg		
2435	2440	2445
Ser Gly Arg Gly Phe Leu Phe Arg Val Leu Arg Ala Ala Leu Pro		
2450	2455	2460
Leu Gln Leu Leu Leu Leu Leu Leu Ile Gly Leu Ala Cys Leu Val		
2465	2470	2475
Pro Met Ser Glu Glu Asp Tyr Ser Cys Ala Leu Ser Asn Asn Phe		
2480	2485	2490
Ala Arg Ser Phe His Pro Met Leu Arg Tyr Thr Asn Gly Pro Pro		
2495	2500	2505
Pro Leu		

<210> 3

<211> 375

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7503554CD1

<400> 3

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala
1 5 10 15

Ile Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro	20	25	30
Arg Leu Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser	35	40	45
Ile Tyr Met Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu	50	55	60
Leu Thr Phe Pro Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu	65	70	75
Leu Gln Thr Asn Asn Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe	80	85	90
Pro Val Asn Leu Thr Gly Leu Asp Leu Ser Gln Asn Asn Leu Ser	95	100	105
Ser Val Thr Asn Ile Asn Val Lys Lys Met Pro Gln Leu Leu Ser	110	115	120
Val Tyr Leu Glu Glu Asn Lys Leu Thr Glu Leu Pro Glu Lys Cys	125	130	135
Leu Ser Glu Leu Ser Asn Leu Gln Glu Leu Tyr Ile Asn His Asn	140	145	150
Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe Ile Gly Leu His Asn	155	160	165
Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu Gln Met Ile Asn	170	175	180
Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile Leu Met Ile	185	190	195
Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe Lys Pro	200	205	210
Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu Thr	215	220	225
Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser	230	235	240
Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala	245	250	255
Leu Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn	260	265	270
Pro Ile Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His	275	280	285
Leu Lys Glu Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile	290	295	300
Asp Ser Leu Ala Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu	305	310	315
Ala Thr Asn Asn Pro Arg Leu Ser Tyr Ile His Pro Asn Ala Phe	320	325	330
Phe Arg Leu Pro Lys Leu Glu Ser Leu Met Leu Asn Ser Asn Ala	335	340	345
Leu Ser Ala Leu Cys His Pro Leu Asp Glu His Glu Gln Asn Gln	350	355	360
His Ser Ile His Gly Ala Arg Phe Thr Val Leu Arg Gly Pro Thr	365	370	375

<210> 4

<211> 340

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506077CD1

<400> 4

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Met Gly Gly Cys Ala Gly Ser Arg Arg Arg Phe Ser Asp Ser Glu
 1          5          10          15
Gly Glu Glu Thr Val Pro Glu Pro Arg Leu Pro Leu Leu Asp His
          20          25          30
Gln Gly Ala His Trp Lys Asn Ala Val Gly Phe Trp Leu Leu Gly
          35          40          45
Leu Cys Asn Asn Phe Ser Tyr Val Val Met Leu Ser Ala Ala His
          50          55          60
Asp Ile Leu Ser His Lys Arg Thr Ser Gly Asn Gln Ser His Val
          65          70          75
Asp Pro Gly Pro Thr Pro Ile Pro His Asn Ser Ser Ser Arg Phe
          80          85          90
Asp Cys Asn Ser Val Ser Thr Ala Leu Ser Tyr Leu Gly Leu Thr
          95          100          105
Gln Ala Gly Leu Ser Pro Gln Gln Thr Leu Leu Ser Met Leu Gly
          110          115          120
Ile Pro Ala Leu Leu Leu Ala Ser Tyr Phe Leu Leu Leu Thr Ser
          125          130          135
Pro Glu Ala Gln Asp Pro Gly Gly Glu Glu Glu Ala Glu Ser Ala
          140          145          150
Ala Arg Gln Pro Leu Ile Arg Thr Glu Ala Pro Glu Ser Lys Pro
          155          160          165
Gly Ser Ser Ser Ser Leu Ser Leu Arg Glu Arg Trp Thr Val Phe
          170          175          180
Lys Gly Leu Leu Trp Tyr Ile Val Pro Leu Val Val Val Tyr Phe
          185          190          195
Ala Glu Tyr Phe Ile Asn Gln Gly Leu Phe Glu Leu Leu Phe Phe
          200          205          210
Trp Asn Thr Ser Leu Ser His Ala Gln Gln Tyr Arg Trp Tyr Gln
          215          220          225
Met Leu Tyr Gln Ala Gly Val Phe Ala Ser Arg Ser Ser Leu Arg
          230          235          240
Cys Cys Arg Ile Arg Phe Thr Trp Ala Leu Ala Leu Leu Gln Cys
          245          250          255
Leu Asn Leu Val Phe Leu Leu Ala Asp Val Trp Phe Gly Phe Leu
          260          265          270
Pro Ser Ile Tyr Leu Val Phe Leu Ile Ile Leu Tyr Glu Gly Leu
          275          280          285
Leu Gly Gly Ala Ala Tyr Val Asn Thr Phe His Asn Ile Ala Leu
          290          295          300
Glu Thr Ser Asp Glu His Arg Glu Phe Ala Met Ala Ala Thr Cys
          305          310          315
Ile Ser Asp Thr Leu Gly Ile Ser Leu Ser Gly Leu Leu Ala Leu
          320          325          330
Pro Leu His Asp Phe Leu Cys Gln Leu Ser
          335          340

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<210> 5

<211> 287

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506765CD1

<400> 5

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Met Ala Leu Gly Leu Leu Ile Ala Val Pro Leu Leu Leu Gln Ala
 1           5           10           15
Ala Pro Arg Gly Ala Ala His Tyr Glu Met Met Gly Thr Cys Arg
          20           25           30
Met Ile Cys Asp Pro Tyr Thr Ala Ala Pro Gly Gly Glu Pro Pro
          35           40           45
Gly Ala Lys Ala Gln Pro Pro Gly Pro Ser Thr Ala Ala Leu Glu
          50           55           60
Val Met Gln Asp Leu Ser Ala Asn Pro Pro Pro Pro Phe Ile Gln
          65           70           75
Gly Pro Lys Gly Asp Pro Gly Arg Pro Gly Lys Pro Gly Pro Arg
          80           85           90
Gly Pro Pro Gly Glu Pro Gly Pro Pro Gly Pro Arg Gly Pro Pro
          95          100          105
Gly Glu Lys Gly Asp Ser Gly Arg Pro Gly Leu Pro Gly Leu Gln
          110         115         120
Leu Thr Ala Gly Thr Ala Ser Gly Val Gly Val Val Gly Gly Gly
          125         130         135
Ala Gly Val Gly Gly Asp Ser Glu Gly Glu Val Thr Ser Ala Leu
          140         145         150
Ser Ala Thr Phe Ser Gly Pro Lys Ile Ala Phe Tyr Val Gly Leu
          155         160         165
Lys Ser Pro His Glu Gly Tyr Glu Val Leu Lys Phe Asp Asp Val
          170         175         180
Val Thr Asn Leu Gly Asn His Tyr Asp Pro Thr Thr Gly Lys Phe
          185         190         195
Ser Cys Gln Val Arg Gly Ile Tyr Phe Phe Thr Tyr His Ile Leu
          200         205         210
Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Cys Lys
          215         220         225
Asn Gly Gln Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln
          230         235         240
Asn Tyr Asp Tyr Ala Ser Asn Ser Val Val Leu His Leu Asp Ser
          245         250         255
Gly Asp Glu Val Tyr Val Lys Leu Asp Gly Gly Lys Ala His Gly
          260         265         270
Gly Asn Asn Asn Lys Tyr Ser Thr Phe Ser Gly Phe Leu Leu Tyr
          275         280         285
Pro Asp

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<210> 6

<211> 1048

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7490048CD1

<400> 6

Met	Leu	Ala	Val	Ser	Leu	Lys	Trp	Arg	Leu	Gly	Val	Val	Arg	Arg	1	5	10	15
Arg	Leu	Lys	Asp	Asp	Gly	Pro	Tyr	Ser	Lys	Gly	Gly	Lys	Asp	Ala	20	25	30	
Gly	Gly	Ala	Asp	Val	Ser	Leu	Ala	Cys	Arg	Arg	Gln	Ser	Ile	Pro	35	40	45	
Glu	Glu	Phe	Arg	Gly	Ile	Thr	Val	Val	Glu	Leu	Ile	Lys	Lys	Glu	50	55	60	
Gly	Ser	Thr	Leu	Gly	Leu	Thr	Ile	Ser	Gly	Gly	Thr	Asp	Lys	Asp	65	70	75	
Gly	Lys	Pro	Arg	Val	Ser	Asn	Leu	Arg	Pro	Gly	Gly	Leu	Ala	Ala	80	85	90	
Arg	Ser	Asp	Leu	Leu	Asn	Ile	Gly	Asp	Tyr	Ile	Arg	Ser	Val	Asn	95	100	105	
Gly	Ile	His	Leu	Thr	Arg	Leu	Arg	His	Asp	Glu	Ile	Ile	Thr	Leu	110	115	120	
Leu	Lys	Asn	Val	Gly	Glu	Arg	Val	Val	Leu	Glu	Val	Glu	Tyr	Glu	125	130	135	
Leu	Pro	Pro	Pro	Ala	Pro	Glu	Asn	Asn	Pro	Arg	Ile	Ile	Ser	Lys	140	145	150	
Thr	Val	Asp	Val	Ser	Leu	Tyr	Lys	Glu	Gly	Asn	Ser	Phe	Gly	Phe	155	160	165	
Val	Leu	Arg	Gly	Gly	Ala	His	Glu	Asp	Gly	His	Lys	Ser	Arg	Pro	170	175	180	
Leu	Val	Leu	Thr	Tyr	Val	Arg	Pro	Gly	Gly	Pro	Ala	Asp	Arg	Glu	185	190	195	
Gly	Ser	Leu	Lys	Val	Gly	Asp	Arg	Leu	Leu	Ser	Val	Asp	Gly	Ile	200	205	210	
Pro	Leu	His	Gly	Ala	Ser	His	Ala	Thr	Ala	Leu	Ala	Thr	Leu	Arg	215	220	225	
Gln	Cys	Ser	His	Glu	Ala	Leu	Phe	Gln	Val	Glu	Tyr	Asp	Val	Ala	230	235	240	
Thr	Pro	Asp	Thr	Val	Ala	Asn	Ala	Ser	Gly	Pro	Leu	Met	Val	Glu	245	250	255	
Ile	Val	Lys	Thr	Pro	Gly	Ser	Ala	Leu	Gly	Ile	Ser	Leu	Thr	Thr	260	265	270	
Thr	Ser	Leu	Arg	Asn	Lys	Ser	Val	Ile	Thr	Ile	Asp	Arg	Ile	Lys	275	280	285	
Pro	Ala	Ser	Val	Val	Asp	Arg	Ser	Gly	Ala	Leu	His	Pro	Gly	Asp	290	295	300	
His	Ile	Leu	Ser	Ile	Asp	Gly	Thr	Ser	Met	Glu	His	Cys	Ser	Leu	305	310	315	
Leu	Glu	Ala	Thr	Lys	Leu	Leu	Ala	Ser	Ile	Ser	Glu	Lys	Val	Arg	320	325	330	
Leu	Glu	Ile	Leu	Pro	Val	Pro	Gln	Ser	Gln	Arg	Pro	Leu	Arg	Pro	335	340	345	
Ser	Glu	Ala	Val	Lys	Val	Gln	Arg	Ser	Glu	Gln	Leu	His	Arg	Trp	350	355	360	
Asp	Pro	Cys	Val	Pro	Ser	Cys	His	Ser	Pro	Arg	Pro	Gly	His	Cys	365	370	375	
Arg	Met	Pro	Thr	Trp	Ala	Thr	Pro	Ala	Gly	Gln	Asp	Gln	Ser	Arg	380	385	390	
Ser	Leu	Ser	Ser	Thr	Pro	Phe	Ser	Ser	Pro	Thr	Leu	Asn	His	Ala	395	400	405	
Phe	Ser	Cys	Asn	Asn	Pro	Ser	Thr	Leu	Pro	Arg	Gly	Ser	Gln	Pro	410	415	420	

Met Ser Pro Arg	Thr Thr Met Gly Arg	Arg Arg His Arg Arg Arg	
	425	430	435
Glu His Lys Thr	Ser Leu Ser Leu Ala	Ser Ser Thr Val Gly Pro	
	440	445	450
Gly Gly Gln Ile	Val His Thr Glu Thr	Thr Glu Val Val Leu Cys	
	455	460	465
Gly Asp Pro Leu	Ser Gly Phe Gly Leu	Gln Leu Gln Gly Gly Ile	
	470	475	480
Phe Ala Thr Glu	Thr Leu Ser Ser Pro	Pro Leu Val Cys Phe Ile	
	485	490	495
Glu Pro Asp Ser	Pro Ala Glu Arg Cys	Gly Leu Leu Gln Val Gly	
	500	505	510
Asp Arg Val Leu	Ser Ile Asn Gly Ile	Ala Thr Glu Asp Gly Thr	
	515	520	525
Met Glu Glu Ala	Asn Gln Leu Leu Arg	Asp Ala Ala Leu Ala His	
	530	535	540
Lys Val Val Leu	Glu Val Glu Phe Asp	Val Ala Glu Ser Val Ile	
	545	550	555
Pro Ser Ser Gly	Thr Phe His Val Lys	Leu Pro Lys Lys Arg Ser	
	560	565	570
Val Glu Leu Gly	Ile Thr Ile Ser Ser	Ala Ser Arg Lys Arg Gly	
	575	580	585
Glu Pro Leu Ile	Ile Ser Asp Ile Lys	Lys Gly Ser Val Ala His	
	590	595	600
Arg Thr Gly Thr	Leu Glu Pro Gly Asp	Lys Leu Leu Ala Ile Asp	
	605	610	615
Asn Ile Arg Leu	Asp Asn Cys Pro Met	Glu Asp Ala Val Gln Ile	
	620	625	630
Leu Arg Gln Cys	Glu Asp Leu Val Lys	Leu Lys Ile Arg Lys Asp	
	635	640	645
Glu Asp Asn Ser	Asp Glu Leu Glu Thr	Thr Gly Ala Val Ser Tyr	
	650	655	660
Thr Val Glu Leu	Lys Arg Tyr Gly Gly	Pro Leu Gly Ile Thr Ile	
	665	670	675
Ser Gly Thr Glu	Glu Pro Phe Asp Pro	Ile Val Ile Ser Gly Leu	
	680	685	690
Thr Lys Arg Gly	Leu Ala Glu Arg Thr	Gly Ala Ile His Val Gly	
	695	700	705
Asp Arg Ile Leu	Ala Ile Asn Asn Val	Ser Leu Lys Gly Arg Pro	
	710	715	720
Leu Ser Glu Ala	Ile His Leu Leu Gln	Val Ala Gly Glu Thr Val	
	725	730	735
Thr Leu Lys Ile	Lys Lys Gln Leu Asp	Arg Pro Leu Leu Pro Arg	
	740	745	750
Lys Ser Gly Ser	Leu Ser Glu Thr Ser	Asp Ala Asp Glu Asp Pro	
	755	760	765
Ala Asp Ala Leu	Lys Gly Gly Leu Pro	Ala Ala Arg Phe Ser Pro	
	770	775	780
Ala Val Pro Ser	Val Asp Ser Ala Val	Glu Ser Trp Asp Ser Ser	
	785	790	795
Ala Thr Glu Gly	Gly Phe Gly Gly Pro	Gly Ser Tyr Thr Pro Gln	
	800	805	810
Ala Ala Ala Arg	Gly Thr Thr Pro Gln	Glu Arg Arg Pro Gly Trp	
	815	820	825
Leu Arg Gly Ser	Pro Pro Pro Thr Glu	Pro Arg Arg Thr Ser Tyr	
	830	835	840

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Thr Pro Thr Pro Ala Asp Glu Ser Phe Pro Glu Glu Glu Glu Glu
845 850 855
Asp Asp Trp Glu Pro Pro Thr Ser Pro Ala Pro Gly Pro Ala Arg
860 865 870
Glu Glu Gly Phe Trp Arg Met Phe Gly Glu Ala Leu Glu Asp Leu
875 880 885
Glu Ser Cys Gly Gln Ser Glu Leu Leu Arg Glu Leu Glu Ala Ser
890 895 900
Ile Met Thr Gly Thr Val Gln Arg Val Ala Leu Glu Gly Arg Pro
905 910 915
Gly His Arg Pro Trp Gln Arg Gly Arg Glu Val Arg Ala Ser Pro
920 925 930
Ala Glu Met Glu Glu Leu Leu Leu Pro Thr Pro Leu Glu Met His
935 940 945
Lys Val Thr Leu His Lys Asp Pro Met Arg His Asp Phe Gly Phe
950 955 960
Ser Val Ser Asp Gly Leu Leu Glu Lys Gly Val Tyr Val His Thr
965 970 975
Val Arg Pro Asp Gly Pro Ala His Arg Gly Gly Leu Gln Pro Phe
980 985 990
Asp Arg Val Leu Gln Val Asn His Val Arg Thr Arg Asp Phe Asp
995 1000 1005
Cys Cys Leu Ala Val Pro Leu Leu Ala Glu Ala Gly Asp Val Leu
1010 1015 1020
Glu Leu Ile Ile Ser Arg Lys Pro His Thr Ala His Ser Ser Arg
1025 1030 1035
Ala Pro Arg Ser Pro Gly Pro Ser Ser Pro Arg Met Leu
1040 1045

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<210> 7

<211> 419

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2133585CD1

<400> 7

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Met Gly Ser Pro Ala His Arg Pro Ala Leu Leu Leu Leu Leu Pro
1 5 10 15
Pro Leu Leu Leu Leu Leu Leu Arg Val Pro Pro Ser Arg Ser
20 25 30
Phe Pro Gly Ser Gly Asp Ser Pro Leu Glu Asp Asp Glu Val Gly
35 40 45
Tyr Ser His Pro Arg Tyr Lys Asp Thr Pro Trp Cys Ser Pro Ile
50 55 60
Lys Val Lys Tyr Gly Asp Val Tyr Cys Arg Ala Pro Gln Gly Gly
65 70 75
Tyr Tyr Lys Thr Ala Leu Gly Thr Arg Cys Asp Ile Arg Cys Gln
80 85 90
Lys Gly Tyr Glu Leu His Gly Ser Ser Leu Leu Ile Cys Gln Ser
95 100 105
Asn Lys Arg Trp Ser Asp Lys Val Ile Cys Arg Gln Lys Arg Cys
110 115 120
Pro Thr Leu Ala Met Pro Ala Asn Gly Gly Phe Lys Cys Val Asp

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	125		130		135									
Gly	Ala	Tyr	Phe	Asn	Ser	Arg	Cys	Glu	Tyr	Tyr	Cys	Ser	Pro	Gly
	140								145					150
Tyr	Thr	Leu	Lys	Gly	Glu	Arg	Thr	Val	Thr	Cys	Met	Asp	Asn	Lys
	155								160					165
Ala	Trp	Ser	Gly	Arg	Pro	Ala	Ser	Cys	Val	Asp	Met	Glu	Pro	Pro
	170								175					180
Arg	Ile	Lys	Cys	Pro	Ser	Val	Lys	Glu	Arg	Ile	Ala	Glu	Pro	Asn
	185								190					195
Lys	Leu	Thr	Val	Arg	Val	Ser	Trp	Glu	Thr	Pro	Glu	Gly	Arg	Asp
	200								205					210
Thr	Ala	Asp	Gly	Ile	Leu	Thr	Asp	Val	Ile	Leu	Lys	Gly	Leu	Pro
	215								220					225
Pro	Gly	Ser	Asn	Phe	Pro	Glu	Gly	Asp	His	Lys	Ile	Gln	Tyr	Thr
	230								235					240
Val	Tyr	Asp	Arg	Ala	Glu	Asn	Lys	Gly	Thr	Cys	Lys	Phe	Arg	Val
	245								250					255
Lys	Val	Arg	Val	Lys	Arg	Cys	Gly	Lys	Leu	Asn	Ala	Pro	Glu	Asn
	260								265					270
Gly	Tyr	Met	Lys	Cys	Ser	Ser	Asp	Gly	Asp	Asn	Tyr	Gly	Ala	Thr
	275								280					285
Cys	Glu	Phe	Ser	Cys	Ile	Gly	Gly	Tyr	Glu	Leu	Gln	Gly	Ser	Pro
	290								295					300
Ala	Arg	Val	Cys	Gln	Ser	Asn	Leu	Ala	Trp	Ser	Gly	Thr	Glu	Pro
	305								310					315
Thr	Cys	Ala	Ala	Met	Asn	Val	Asn	Val	Gly	Val	Arg	Thr	Ala	Ala
	320								325					330
Ala	Leu	Leu	Asp	Gln	Phe	Tyr	Glu	Lys	Arg	Arg	Leu	Leu	Ile	Val
	335								340					345
Ser	Thr	Pro	Thr	Ala	Arg	Asn	Leu	Leu	Tyr	Arg	Leu	Gln	Leu	Gly
	350								355					360
Met	Leu	Gln	Gln	Ala	Gln	Cys	Gly	Leu	Asp	Leu	Arg	His	Ile	Thr
	365								370					375
Val	Val	Glu	Leu	Val	Gly	Val	Phe	Pro	Thr	Leu	Ile	Gly	Arg	Ile
	380								385					390
Gly	Ala	Lys	Ile	Met	Pro	Pro	Ala	Leu	Ala	Leu	Gln	Leu	Ser	Phe
	395								400					405
Ile	Thr	Leu	Thr	Lys	Leu	Glu	Pro	Trp	Ile	Leu	Val	Ser	Glu	
	410								415					

<210> 8

<211> 1109

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509063CD1

<400> 8

Met	Arg	Cys	Lys	Glu	Leu	Glu	Asn	Ala	Val	Gly	Ser	Trp	Thr	Asp
1				5					10					15
Asp	Leu	Thr	Gln	Leu	Ser	Leu	Leu	Lys	Asp	Thr	Leu	Ser	Ala	Tyr
				20					25					30
Ile	Ser	Ala	Asp	Asp	Ile	Ser	Ile	Leu	Asn	Glu	Arg	Val	Glu	Leu
				35					40					45

Leu	Gln	Arg	Gln	Trp	Glu	Glu	Leu	Cys	His	Gln	Leu	Ser	Leu	Arg	50	55	60
Arg	Gln	Gln	Ile	Gly	Glu	Arg	Leu	Asn	Glu	Trp	Ala	Val	Phe	Ser	65	70	75
Glu	Lys	Asn	Lys	Glu	Leu	Cys	Glu	Trp	Leu	Thr	Gln	Met	Glu	Ser	80	85	90
Lys	Val	Ser	Gln	Asn	Gly	Asp	Ile	Leu	Ile	Glu	Glu	Met	Ile	Glu	95	100	105
Lys	Leu	Lys	Lys	Asp	Tyr	Gln	Glu	Glu	Ile	Ala	Ile	Ala	Gln	Glu	110	115	120
Asn	Lys	Ile	Gln	Leu	Gln	Gln	Met	Gly	Glu	Arg	Leu	Ala	Lys	Ala	125	130	135
Ser	His	Glu	Ser	Lys	Ala	Ser	Glu	Ile	Glu	Tyr	Lys	Leu	Gly	Lys	140	145	150
Val	Asn	Asp	Arg	Trp	Gln	His	Leu	Leu	Asp	Leu	Ile	Ala	Ala	Arg	155	160	165
Val	Lys	Lys	Leu	Lys	Glu	Thr	Leu	Val	Ala	Val	Gln	Gln	Leu	Asp	170	175	180
Lys	Asn	Met	Ser	Ser	Leu	Arg	Thr	Trp	Leu	Ala	His	Ile	Glu	Ser	185	190	195
Glu	Leu	Ala	Lys	Pro	Ile	Val	Tyr	Asp	Ser	Cys	Asn	Ser	Glu	Glu	200	205	210
Ile	Gln	Arg	Lys	Leu	Asn	Glu	Gln	Gln	Glu	Leu	Gln	Arg	Asp	Ile	215	220	225
Glu	Lys	His	Ser	Thr	Gly	Val	Ala	Ser	Val	Leu	Asn	Leu	Cys	Glu	230	235	240
Val	Leu	Leu	His	Asp	Cys	Asp	Ala	Cys	Ala	Thr	Asp	Ala	Glu	Cys	245	250	255
Asp	Ser	Ile	Gln	Gln	Ala	Thr	Arg	Asn	Leu	Asp	Arg	Arg	Trp	Arg	260	265	270
Asn	Ile	Cys	Ala	Met	Ser	Met	Glu	Arg	Arg	Leu	Lys	Ile	Glu	Glu	275	280	285
Thr	Trp	Arg	Leu	Trp	Gln	Lys	Phe	Leu	Asp	Asp	Tyr	Ser	Arg	Phe	290	295	300
Glu	Asp	Trp	Leu	Lys	Ser	Ser	Glu	Arg	Thr	Ala	Ala	Phe	Pro	Ser	305	310	315
Ser	Ser	Gly	Val	Ile	Tyr	Thr	Val	Ala	Lys	Glu	Glu	Leu	Lys	Lys	320	325	330
Phe	Glu	Ala	Phe	Gln	Arg	Gln	Val	His	Glu	Cys	Leu	Thr	Gln	Leu	335	340	345
Glu	Leu	Ile	Asn	Lys	Gln	Tyr	Arg	Arg	Leu	Ala	Arg	Glu	Asn	Arg	350	355	360
Thr	Asp	Ser	Ala	Cys	Ser	Leu	Lys	Gln	Met	Val	His	Glu	Gly	Asn	365	370	375
Gln	Arg	Trp	Asp	Asn	Leu	Gln	Lys	Arg	Val	Thr	Ser	Ile	Leu	Arg	380	385	390
Arg	Leu	Lys	His	Phe	Ile	Gly	Gln	Arg	Glu	Glu	Phe	Glu	Thr	Ala	395	400	405
Arg	Asp	Ser	Ile	Leu	Val	Trp	Leu	Thr	Glu	Met	Asp	Leu	Gln	Leu	410	415	420
Thr	Asn	Ile	Glu	His	Phe	Ser	Glu	Cys	Asp	Val	Gln	Ala	Lys	Ile	425	430	435
Lys	Gln	Leu	Lys	Ala	Phe	Gln	Gln	Glu	Ile	Ser	Leu	Asn	His	Asn	440	445	450
Lys	Ile	Glu	Gln	Ile	Ile	Ala	Gln	Gly	Glu	Gln	Leu	Ile	Glu	Lys	455	460	465

Ser Glu Pro Leu Asp Ala Ala Ile Ile Glu Glu Glu Leu Asp Glu	470	475	480
Leu Arg Arg Tyr Cys Gln Glu Val Phe Gly Arg Val Glu Arg Tyr	485	490	495
His Lys Lys Leu Ile Arg Leu Pro Leu Pro Asp Asp Glu His Asp	500	505	510
Leu Ser Asp Arg Glu Leu Glu Leu Glu Asp Ser Ala Ala Leu Ser	515	520	525
Asp Leu His Trp His Asp Arg Ser Ala Asp Ser Leu Leu Ser Pro	530	535	540
Gln Pro Ser Ser Asn Leu Ser Leu Ser Leu Ala Gln Pro Leu Arg	545	550	555
Ser Glu Arg Ser Gly Arg Asp Thr Pro Ala Ser Val Asp Ser Ile	560	565	570
Pro Leu Glu Trp Asp His Asp Tyr Asp Leu Ser Arg Asp Leu Glu	575	580	585
Ser Ala Met Ser Arg Ala Leu Pro Ser Glu Asp Glu Glu Gly Gln	590	595	600
Asp Asp Lys Asp Phe Tyr Leu Arg Gly Ala Val Ala Leu Ser Asp	605	610	615
Val Met Ile Pro Glu Ser Pro Glu Ala Tyr Val Lys Leu Thr Glu	620	625	630
Asn Ala Ile Lys Asn Thr Ser Gly Asp His Ser Ala Leu Glu Ser	635	640	645
Gln Ile Arg Gln Leu Gly Lys Ala Leu Asp Asp Ser Arg Phe Gln	650	655	660
Ile Gln Gln Thr Glu Asn Ile Ile Arg Ser Lys Thr Pro Thr Gly	665	670	675
Pro Glu Leu Asp Thr Ser Tyr Lys Gly Tyr Met Lys Leu Leu Gly	680	685	690
Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg Leu Glu His Lys	695	700	705
Leu Lys Glu Glu Glu Glu Ser Leu Pro Gly Phe Val Asn Leu His	710	715	720
Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp Glu Leu	725	730	735
Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln Asn	740	745	750
Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp	755	760	765
Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg	770	775	780
Leu Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys	785	790	795
Lys Leu Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile	800	805	810
Ile Leu Ser Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp	815	820	825
Ser Lys Glu Ser Arg Asp Leu Gln Asp Arg Leu Ser Gln Met Asn	830	835	840
Gly Arg Trp Asp Arg Val Cys Ser Leu Leu Glu Glu Trp Arg Gly	845	850	855
Leu Leu Gln Asp Ala Leu Met Gln Cys Gln Gly Phe His Glu Met	860	865	870
Ser His Gly Leu Leu Leu Met Leu Glu Asn Ile Asp Arg Arg Lys	875	880	885

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Asn Glu Ile Val Pro Ile Asp Ser Asn Leu Asp Ala Glu Ile Leu
      890                      895                      900
Gln Asp His His Lys Gln Leu Met Gln Ile Lys His Glu Leu Leu
      905                      910                      915
Glu Ser Gln Leu Arg Val Ala Ser Leu Gln Asp Met Ser Cys Gln
      920                      925                      930
Leu Leu Val Asn Ala Glu Gly Thr Asp Cys Leu Glu Ala Lys Glu
      935                      940                      945
Lys Val His Val Ile Gly Asn Arg Leu Lys Leu Leu Leu Lys Glu
      950                      955                      960
Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu Asp Val Ser
      965                      970                      975
Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp Glu Leu
      980                      985                      990
Asp Thr Ser Gly Ser Val Ser Pro Thr Ser Gly Arg Ser Thr Pro
      995                      1000                     1005
Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro
      1010                     1015                     1020
Gly Pro Ser Val Ser Ser Pro His Ser Arg Ser Thr Lys Gly Gly
      1025                     1030                     1035
Ser Asp Ser Ser Leu Ser Glu Pro Gly Pro Gly Arg Ser Gly Arg
      1040                     1045                     1050
Gly Phe Leu Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu
      1055                     1060                     1065
Leu Leu Leu Leu Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser
      1070                     1075                     1080
Glu Glu Asp Tyr Ser Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser
      1085                     1090                     1095
Phe His Pro Met Leu Arg Tyr Thr Asn Gly Pro Pro Pro Leu
      1100                     1105

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<211> 1308

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5496710CD1

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Ser Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser Tyr Asp
      20                      25                      30
Cys Asp Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe Ser
      35                      40                      45
Ser Ser Ser Glu Leu Ser Ser Ser His Gly Pro Gly Phe Ala Arg
      50                      55                      60
Leu Asn Arg Arg Asp Gly Ala Gly Gly Trp Ser Pro Leu Val Ser
      65                      70                      75
Asn Lys Tyr Gln Trp Leu Gln Ile Asp Leu Gly Glu Arg Met Glu
      80                      85                      90
Val Thr Ala Val Ala Thr Gln Gly Gly Tyr Gly Ser Ser Asn Trp
      95                      100                     105
Val Thr Ser Tyr Leu Leu Met Phe Ser Asp Ser Gly Trp Asn Trp

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110	115	120
Lys Gln Tyr Arg Gln Glu Asp Ser Ile Trp Gly Phe Ser Gly Asn		
125	130	135
Ala Asn Ala Asp Ser Val Val Tyr Tyr Arg Leu Gln Pro Ser Ile		
140	145	150
Lys Ala Arg Phe Leu Arg Phe Ile Pro Leu Glu Trp Asn Pro Lys		
155	160	165
Gly Arg Ile Gly Met Arg Ile Glu Val Phe Gly Cys Ala Tyr Arg		
170	175	180
Ser Glu Val Val Asp Leu Asp Gly Lys Ser Ser Leu Leu Tyr Arg		
185	190	195
Phe Asp Gln Lys Ser Leu Ser Pro Ile Lys Asp Ile Ile Ser Leu		
200	205	210
Lys Phe Lys Thr Met Gln Ser Asp Gly Ile Leu Leu His Arg Glu		
215	220	225
Gly Pro Asn Gly Asp His Ile Thr Leu Gln Leu Arg Arg Ala Arg		
230	235	240
Leu Phe Leu Leu Ile Asn Ser Gly Glu Ala Lys Leu Pro Ser Thr		
245	250	255
Ser Thr Leu Val Asn Leu Thr Leu Gly Ser Leu Leu Asp Asp Gln		
260	265	270
His Trp His Ser Val Leu Ile Gln Arg Leu Gly Lys Gln Val Asn		
275	280	285
Phe Thr Val Asp Glu His Arg His His Phe His Ala Arg Gly Glu		
290	295	300
Phe Asn Leu Met Asn Leu Asp Tyr Glu Ile Ser Phe Gly Gly Ile		
305	310	315
Pro Ala Pro Gly Lys Ser Val Ser Phe Pro His Arg Asn Phe His		
320	325	330
Gly Cys Leu Glu Asn Leu Tyr Tyr Asn Gly Val Asp Ile Ile Asp		
335	340	345
Leu Ala Lys Gln Gln Lys Pro Gln Ile Ile Ala Met Gly Asn Val		
350	355	360
Ser Phe Ser Cys Ser Gln Pro Gln Ser Met Pro Val Thr Phe Leu		
365	370	375
Ser Ser Arg Ser Tyr Leu Ala Leu Pro Asp Phe Ser Gly Glu Glu		
380	385	390
Glu Val Ser Ala Thr Phe Gln Phe Arg Thr Trp Asn Lys Ala Gly		
395	400	405
Leu Leu Leu Phe Ser Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu		
410	415	420
Leu Phe Leu Ser Asp Gly Lys Leu Lys Ser Asn Leu Tyr Gln Pro		
425	430	435
Gly Lys Leu Pro Ser Asp Ile Thr Ala Gly Val Glu Leu Asn Asp		
440	445	450
Gly Gln Trp His Ser Val Ser Leu Ser Ala Lys Lys Asn His Leu		
455	460	465
Ser Val Ala Val Asp Gly Gln Met Ala Ser Ala Ala Pro Leu Leu		
470	475	480
Gly Pro Glu Gln Ile Tyr Ser Gly Gly Thr Tyr Tyr Phe Gly Gly		
485	490	495
Cys Pro Asp Lys Ser Phe Gly Ser Lys Cys Lys Ser Pro Leu Gly		
500	505	510
Gly Phe Gln Gly Cys Met Arg Leu Ile Ser Ile Ser Gly Lys Val		
515	520	525
Val Asp Leu Ile Ser Val Gln Gln Gly Ser Leu Gly Asn Phe Ser		

530	535	540
Asp Leu Gln Ile Asp Ser Cys Gly Ile	Ser Asp Arg Cys Leu Pro	
545	550	555
Asn Tyr Cys Glu His Gly Gly Glu Cys	Ser Gln Ser Trp Ser Thr	
560	565	570
Phe His Cys Asn Cys Thr Asn Thr Gly	Tyr Arg Gly Ala Thr Cys	
575	580	585
His Asn Ser Ile Tyr Glu Gln Ser Cys	Glu Ala Tyr Lys His Arg	
590	595	600
Gly Asn Thr Ser Gly Phe Tyr Tyr Ile	Asp Ser Asp Gly Ser Gly	
605	610	615
Pro Leu Glu Pro Phe Leu Leu Tyr Cys	Asn Met Thr Glu Thr Ala	
620	625	630
Trp Thr Ile Ile Gln His Asn Gly Ser	Asp Leu Thr Arg Val Arg	
635	640	645
Asn Thr Asn Pro Glu Asn Pro Tyr Ala	Gly Phe Phe Glu Tyr Val	
650	655	660
Ala Ser Met Glu Gln Leu Gln Ala Thr	Ile Asn Arg Ala Glu His	
665	670	675
Cys Glu Gln Glu Phe Thr Tyr Tyr Cys	Lys Lys Ser Arg Leu Val	
680	685	690
Asn Lys Gln Asp Gly Thr Pro Leu Ser	Trp Trp Val Gly Arg Thr	
695	700	705
Asn Glu Thr Gln Thr Tyr Trp Gly Gly	Ser Ser Pro Asp Leu Gln	
710	715	720
Lys Cys Thr Cys Gly Leu Glu Gly Asn	Cys Ile Asp Ser Gln Tyr	
725	730	735
Tyr Cys Asn Cys Asp Ala Asp Arg Asn	Glu Trp Thr Asn Asp Thr	
740	745	750
Gly Leu Leu Ala Tyr Lys Glu His Leu	Pro Val Thr Lys Ile Val	
755	760	765
Ile Thr Asp Thr Gly Arg Leu His Ser	Glu Ala Ala Tyr Lys Leu	
770	775	780
Gly Pro Leu Leu Cys Arg Gly Asp Arg	Ser Phe Trp Asn Ser Ala	
785	790	795
Ser Phe Asp Thr Glu Ala Ser Tyr Leu	His Phe Pro Thr Phe His	
800	805	810
Gly Glu Leu Ser Ala Asp Val Ser Phe	Phe Phe Lys Thr Thr Ala	
815	820	825
Ser Ser Gly Val Phe Leu Glu Asn Leu	Gly Ile Ala Asp Phe Ile	
830	835	840
Arg Ile Glu Leu Arg Ser Pro Thr Val	Val Thr Phe Ser Phe Asp	
845	850	855
Val Gly Asn Gly Pro Phe Glu Ile Ser	Val Gln Ser Pro Thr His	
860	865	870
Phe Asn Asp Asn Gln Trp His His Val	Arg Val Glu Arg Asn Met	
875	880	885
Lys Glu Ala Ser Leu Gln Val Asp Gln	Leu Thr Pro Lys Thr Gln	
890	895	900
Pro Ala Pro Ala Asp Gly His Val Leu	Leu Gln Leu Asn Ser Gln	
905	910	915
Leu Phe Val Gly Gly Thr Ala Thr Arg	Gln Arg Gly Phe Leu Gly	
920	925	930
Cys Ile Arg Ser Leu Gln Leu Asn Gly	Met Thr Leu Asp Leu Glu	
935	940	945
Glu Arg Ala Gln Val Thr Pro Glu Val	Gln Pro Gly Cys Arg Gly	

	950		955		960
His Cys Ser Ser	Tyr Gly Lys Leu Cys Arg Asn Gly Gly Lys Cys				
	965		970		975
Arg Glu Arg Pro	Ile Gly Phe Phe Cys Asp Cys Thr Phe Ser Ala				
	980		985		990
Tyr Thr Gly Pro	Phe Cys Ser Asn Glu Ile Ser Ala Tyr Phe Gly				
	995		1000		1005
Ser Gly Ser Ser	Val Ile Tyr Asn Phe Gln Glu Asn Tyr Leu Leu				
	1010		1015		1020
Ser Lys Asn Ser Ser	Ser His Ala Ala Ser Phe His Gly Asp Met				
	1025		1030		1035
Lys Leu Ser Arg	Glu Met Ile Lys Phe Ser Phe Arg Thr Thr Arg				
	1040		1045		1050
Thr Pro Ser Leu	Leu Leu Phe Val Ser Ser Phe Tyr Lys Glu Tyr				
	1055		1060		1065
Leu Ser Val Ile	Ile Ala Lys Asn Gly Ser Leu Gln Ile Arg Tyr				
	1070		1075		1080
Lys Leu Asn Lys	Tyr Gln Glu Pro Asp Val Val Asn Phe Asp Phe				
	1085		1090		1095
Lys Asn Met Ala	Asp Gly Gln Leu His His Ile Met Ile Asn Arg				
	1100		1105		1110
Glu Glu Gly Val	Val Phe Ile Glu Ile Asp Asp Asn Arg Arg Arg				
	1115		1120		1125
Gln Val His Leu	Ser Ser Gly Thr Glu Phe Ser Ala Val Lys Ser				
	1130		1135		1140
Leu Val Leu Gly	Arg Ile Leu Glu His Ser Asp Val Asp Gln Asp				
	1145		1150		1155
Thr Ala Leu Ala	Gly Ala Gln Gly Phe Thr Gly Cys Leu Ser Ala				
	1160		1165		1170
Val Gln Leu Ser	His Val Ala Pro Leu Lys Ala Ala Leu His Pro				
	1175		1180		1185
Ser His Pro Asp	Pro Val Thr Val Thr Gly His Val Thr Glu Ser				
	1190		1195		1200
Ser Cys Met Ala	Gln Pro Gly Thr Asp Ala Thr Ser Arg Glu Arg				
	1205		1210		1215
Thr His Ser Phe	Ala Asp His Ser Gly Thr Ile Asp Asp Arg Glu				
	1220		1225		1230
Pro Leu Ala Asn	Ala Ile Lys Ser Asp Ser Ala Val Ile Gly Gly				
	1235		1240		1245
Leu Ile Ala Val	Val Ile Phe Ile Leu Leu Cys Ile Thr Ala Ile				
	1250		1255		1260
Ala Val Arg Ile	Tyr Gln Gln Lys Arg Leu Tyr Lys Arg Ser Glu				
	1265		1270		1275
Ala Lys Arg Ser	Glu Asn Val Asp Ser Ala Glu Ala Val Leu Lys				
	1280		1285		1290
Ser Glu Leu Asn	Ile Gln Asn Ala Val Asn Glu Asn Gln Lys Glu				
	1295		1300		1305
Tyr Phe Phe					

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<211> 1009

<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 72150826CD1

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Met Asp Leu Ile Arg Gly Val Leu Leu Arg Leu Leu Leu Leu Ala
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Ser Ser Leu Gly Pro Gly Ala Val Ser Leu Arg Ala Ala Ile Arg
              20              25              30
Lys Pro Gly Lys Val Gly Pro Pro Leu Asp Ile Lys Leu Gly Ala
              35              40              45
Leu Asn Cys Thr Ala Phe Ser Ile Gln Trp Lys Met Pro Arg His
              50              55              60
Pro Gly Ser Pro Ile Leu Gly Tyr Thr Val Phe Tyr Ser Glu Val
              65              70              75
Gly Ala Asp Lys Ser Leu Gln Glu Gln Leu His Ser Val Pro Leu
              80              85              90
Ser Arg Asp Ile Pro Thr Thr Glu Glu Val Ile Gly Asp Leu Lys
              95              100             105
Pro Gly Thr Glu Tyr His Val Ser Ile Ala Ala Tyr Ser Gln Ala
              110             115             120
Gly Lys Gly Arg Leu Ser Ser Pro Arg His Val Thr Thr Leu Ser
              125             130             135
Gln Asp Ser Cys Leu Pro Pro Ala Ala Pro Gln Gln Pro His Val
              140             145             150
Ile Val Val Ser Asp Ser Glu Val Ala Leu Ser Trp Lys Pro Gly
              155             160             165
Ala Ser Glu Gly Ser Ala Pro Ile Gln Tyr Tyr Ser Val Glu Phe
              170             175             180
Ile Arg Pro Asp Phe Asp Lys Lys Trp Thr Ser Ile His Glu Arg
              185             190             195
Ile Gln Met Asp Ser Met Val Ile Lys Gly Leu Asp Pro Asp Thr
              200             205             210
Asn Tyr Gln Phe Ala Val Arg Ala Met Asn Ser His Gly Pro Ser
              215             220             225
Pro Arg Ser Trp Pro Ser Asp Ile Ile Arg Thr Leu Cys Pro Glu
              230             235             240
Glu Ala Gly Ser Gly Arg Tyr Gly Pro Arg Tyr Ile Thr Asp Met
              245             250             255
Gly Ala Gly Glu Asp Asp Glu Gly Phe Glu Asp Asp Leu Asp Leu
              260             265             270
Asp Ile Ser Phe Glu Glu Val Lys Pro Leu Pro Ala Thr Lys Gly
              275             280             285
Gly Asn Lys Lys Phe Leu Val Glu Ser Lys Lys Met Ser Ile Ser
              290             295             300
Asn Pro Lys Thr Ile Ser Arg Leu Ile Pro Pro Thr Ser Ala Ser
              305             310             315
Leu Pro Val Thr Thr Val Ala Pro Gln Pro Ile Pro Ile Gln Arg
              320             325             330
Lys Gly Lys Asn Gly Val Ala Ile Met Ser Arg Leu Phe Asp Met
              335             340             345
Pro Cys Asp Glu Thr Leu Cys Ser Ala Asp Ser Phe Cys Val Asn
              350             355             360
Asp Tyr Thr Trp Gly Gly Ser Arg Cys Gln Cys Thr Leu Gly Lys
              365             370             375
Gly Gly Glu Ser Cys Ser Glu Asp Ile Val Ile Gln Tyr Pro Gln
              380             385             390

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Phe	Phe	Gly	His	Ser	Tyr	Val	Thr	Phe	Glu	Pro	Leu	Lys	Asn	Ser	395	400	405
Tyr	Gln	Ala	Phe	Gln	Ile	Thr	Leu	Glu	Phe	Arg	Ala	Glu	Ala	Glu	410	415	420
Asp	Gly	Leu	Leu	Leu	Tyr	Cys	Gly	Glu	Asn	Glu	His	Gly	Arg	Gly	425	430	435
Asp	Phe	Met	Ser	Leu	Ala	Ile	Ile	Arg	Arg	Ser	Leu	Gln	Phe	Arg	440	445	450
Phe	Asn	Cys	Gly	Thr	Gly	Val	Ala	Ile	Ile	Val	Ser	Glu	Thr	Lys	455	460	465
Ile	Lys	Leu	Gly	Gly	Trp	His	Thr	Val	Met	Leu	Tyr	Arg	Asp	Gly	470	475	480
Leu	Asn	Gly	Leu	Leu	Gln	Leu	Asn	Asn	Gly	Thr	Pro	Val	Thr	Gly	485	490	495
Gln	Ser	Gln	Gly	Gln	Tyr	Ser	Lys	Ile	Thr	Phe	Arg	Thr	Pro	Leu	500	505	510
Tyr	Leu	Gly	Gly	Ala	Pro	Ser	Ala	Tyr	Trp	Leu	Val	Arg	Ala	Thr	515	520	525
Gly	Thr	Asn	Arg	Gly	Phe	Gln	Gly	Cys	Val	Gln	Ser	Leu	Ala	Val	530	535	540
Asn	Gly	Arg	Arg	Ile	Asp	Met	Arg	Pro	Trp	Pro	Leu	Gly	Lys	Ala	545	550	555
Leu	Ser	Gly	Ala	Asp	Val	Gly	Glu	Cys	Ser	Ser	Gly	Ile	Cys	Asp	560	565	570
Glu	Ala	Ser	Cys	Ile	His	Gly	Gly	Thr	Cys	Thr	Ala	Ile	Lys	Ala	575	580	585
Asp	Ser	Tyr	Ile	Cys	Leu	Cys	Pro	Leu	Gly	Phe	Lys	Gly	Arg	His	590	595	600
Cys	Glu	Asp	Ala	Phe	Thr	Leu	Thr	Ile	Pro	Gln	Phe	Arg	Glu	Ser	605	610	615
Leu	Arg	Ser	Tyr	Ala	Ala	Thr	Pro	Trp	Pro	Leu	Glu	Pro	Gln	His	620	625	630
Tyr	Leu	Ser	Phe	Met	Glu	Phe	Glu	Ile	Thr	Phe	Arg	Pro	Asp	Ser	635	640	645
Gly	Asp	Gly	Val	Leu	Leu	Tyr	Ser	Tyr	Asp	Thr	Gly	Ser	Lys	Asp	650	655	660
Phe	Leu	Ser	Ile	Asn	Leu	Ala	Gly	Gly	His	Val	Glu	Phe	Arg	Phe	665	670	675
Asp	Cys	Gly	Ser	Gly	Thr	Gly	Val	Leu	Arg	Ser	Glu	Asp	Pro	Leu	680	685	690
Thr	Leu	Gly	Asn	Trp	His	Glu	Leu	Arg	Val	Ser	Arg	Thr	Ala	Lys	695	700	705
Asn	Gly	Ile	Leu	Gln	Val	Asp	Lys	Gln	Lys	Ile	Val	Glu	Gly	Met	710	715	720
Ala	Glu	Gly	Gly	Phe	Thr	Gln	Ile	Lys	Cys	Asn	Thr	Asp	Ile	Phe	725	730	735
Ile	Gly	Gly	Val	Pro	Asn	Tyr	Asp	Asp	Val	Lys	Lys	Asn	Ser	Gly	740	745	750
Val	Leu	Lys	Pro	Phe	Ser	Gly	Ser	Ile	Gln	Lys	Ile	Ile	Leu	Asn	755	760	765
Asp	Arg	Thr	Ile	His	Val	Lys	His	Asp	Phe	Thr	Ser	Gly	Val	Asn	770	775	780
Val	Glu	Asn	Ala	Ala	His	Pro	Cys	Val	Arg	Ala	Pro	Cys	Ala	His	785	790	795
Gly	Gly	Ser	Cys	Arg	Pro	Arg	Lys	Glu	Gly	Tyr	Asp	Cys	Asp	Cys	800	805	810

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Pro Leu Gly Phe Glu Gly Leu His Cys Gln Lys Ala Ile Ile Glu
      815                      820                      825
Ala Ile Glu Ile Pro Gln Phe Ile Gly Arg Ser Tyr Leu Thr Tyr
      830                      835                      840
Asp Asn Pro Asp Ile Leu Lys Arg Val Ser Gly Ser Arg Ser Asn
      845                      850                      855
Val Phe Met Arg Phe Lys Thr Thr Ala Lys Asp Gly Leu Leu Leu
      860                      865                      870
Trp Arg Gly Asp Ser Pro Met Arg Pro Asn Ser Asp Phe Ile Ser
      875                      880                      885
Leu Gly Leu Arg Asp Gly Ala Leu Val Phe Ser Tyr Asn Leu Gly
      890                      895                      900
Ser Gly Val Ala Ser Ile Met Val Asn Gly Ser Phe Asn Asp Gly
      905                      910                      915
Arg Trp His Arg Val Lys Ala Val Arg Asp Gly Gln Ser Gly Lys
      920                      925                      930
Ile Thr Val Asp Asp Tyr Gly Ala Arg Thr Gly Lys Ser Pro Gly
      935                      940                      945
Met Met Arg Gln Leu Asn Ile Asn Gly Ala Leu Tyr Val Gly Gly
      950                      955                      960
Met Lys Glu Ile Ala Leu His Thr Asn Arg Gln Tyr Met Arg Gly
      965                      970                      975
Leu Val Gly Cys Ile Ser His Phe Thr Leu Ser Thr Asp Tyr His
      980                      985                      990
Ile Ser Leu Val Glu Asp Ala Val Asp Gly Lys Asn Ile Asn Thr
      995                      1000                     1005
Cys Gly Ala Lys

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<210> 11

<211> 962

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 6799476CD1

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Met Leu Arg Arg Pro Ala Pro Ala Leu Ala Pro Ala Ala Arg Leu
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Leu Leu Ala Gly Leu Leu Cys Gly Gly Gly Val Trp Ala Ala Arg
      20                      25                      30
Val Asn Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly Ile
      35                      40                      45
Val Thr Glu Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu Ile
      50                      55                      60
Ala Leu Asp Lys Asp Ala Pro Leu Arg Phe Ala Glu Ser Phe Glu
      65                      70                      75
Val Thr Val Thr Lys Glu Gly Glu Ile Cys Gly Phe Lys Ile His
      80                      85                      90
Gly Gln Asn Val Pro Phe Asp Ala Val Val Val Asp Lys Ser Thr
      95                      100                     105
Gly Glu Gly Val Ile Arg Ser Lys Glu Lys Leu Asp Cys Glu Leu
      110                     115                     120
Gln Lys Asp Tyr Ser Phe Thr Ile Gln Ala Tyr Asp Cys Gly Lys

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	125	130	135
Gly Pro Asp Gly	Thr Asn Val Lys Lys	Ser His Lys Ala Thr	Val
	140	145	150
His Ile Gln Val	Asn Asp Val Asn Glu Tyr	Ala Pro Val Phe	Lys
	155	160	165
Glu Lys Ser Tyr	Lys Ala Thr Val Ile	Glu Gly Lys Gln Tyr	Asp
	170	175	180
Ser Ile Leu Arg	Val Glu Ala Val Asp	Ala Asp Cys Ser Pro	Gln
	185	190	195
Phe Ser Gln Ile	Cys Ser Tyr Glu Ile	Ile Thr Pro Asp Val	Pro
	200	205	210
Phe Thr Val Asp	Lys Asp Gly Tyr Ile	Lys Asn Thr Glu Lys	Leu
	215	220	225
Asn Tyr Gly Lys	Glu His Gln Tyr Lys	Leu Thr Val Thr Ala	Tyr
	230	235	240
Asp Cys Gly Lys	Lys Arg Ala Thr Glu	Asp Val Leu Val Lys	Ile
	245	250	255
Ser Ile Lys Pro	Thr Cys Thr Pro Gly	Trp Gln Gly Trp Asn	Asn
	260	265	270
Arg Ile Glu Tyr	Glu Pro Gly Thr Gly	Ala Leu Ala Val Phe	Pro
	275	280	285
Asn Ile His Leu	Glu Thr Cys Asp Glu	Pro Val Ala Ser Val	Gln
	290	295	300
Ala Thr Val Glu	Leu Glu Thr Ser His	Ile Gly Lys Gly Cys	Asp
	305	310	315
Arg Asp Thr Tyr	Ser Glu Lys Ser Leu	His Arg Leu Cys Gly	Ala
	320	325	330
Ala Ala Gly Thr	Ala Glu Leu Leu Pro	Ser Pro Ser Gly Ser	Leu
	335	340	345
Asn Trp Thr Met	Gly Leu Pro Thr Asp	Asn Gly His Asp Ser	Asp
	350	355	360
Gln Val Phe Glu	Phe Asn Gly Thr Gln	Ala Val Arg Ile Pro	Asp
	365	370	375
Gly Val Val Ser	Val Ser Pro Lys Glu	Pro Phe Thr Ile Ser	Val
	380	385	390
Trp Met Arg His	Gly Pro Phe Gly Arg	Lys Lys Glu Thr Ile	Leu
	395	400	405
Cys Ser Ser Asp	Lys Thr Asp Met Asn	Arg His His Tyr Ser	Leu
	410	415	420
Tyr Val His Gly	Cys Arg Leu Ile Phe	Leu Phe Arg Gln Asp	Pro
	425	430	435
Ser Glu Glu Lys	Lys Tyr Arg Pro Ala	Glu Phe His Trp Lys	Leu
	440	445	450
Asn Gln Val Cys	Asp Glu Glu Trp His	His Tyr Val Leu Asn	Val
	455	460	465
Glu Phe Pro Ser	Val Thr Leu Tyr Val	Asp Gly Thr Ser His	Glu
	470	475	480
Pro Phe Ser Val	Thr Glu Asp Tyr Pro	Leu His Pro Ser Lys	Ile
	485	490	495
Glu Thr Gln Leu	Val Val Gly Ala Cys	Trp Gln Gly Gly Asp	Leu
	500	505	510
His Met Thr Gln	Phe Phe Arg Gly Asn	Leu Ala Gly Leu Thr	Leu
	515	520	525
Arg Ser Gly Lys	Leu Ala Asp Lys Lys	Val Ile Asp Cys Leu	Tyr
	530	535	540
Thr Cys Lys Glu	Gly Leu Asp Leu Gln	Val Leu Glu Asp Ser	Gly

545	550	555
Arg Gly Val Gln	Ile Gln Ala His Pro	Ser Gln Leu Val Leu Thr
560	565	570
Leu Glu Gly Glu	Asp Leu Gly Glu Leu	Asp Lys Ala Met Gln His
575	580	585
Ile Ser Tyr Leu	Asn Ser Arg Gln Phe	Pro Thr Pro Gly Ile Arg
590	595	600
Arg Leu Lys Ile	Thr Ser Thr Ile Lys	Cys Phe Asn Glu Ala Thr
605	610	615
Cys Ile Ser Val	Pro Pro Val Asp Gly	Tyr Val Met Val Leu Gln
620	625	630
Pro Glu Glu Pro	Lys Ile Ser Leu Ser	Gly Val His His Phe Ala
635	640	645
Arg Ala Ala Ser	Glu Phe Glu Ser Ser	Glu Gly Val Phe Leu Phe
650	655	660
Pro Glu Leu Arg	Ile Ile Ser Thr Ile	Thr Arg Glu Val Glu Pro
665	670	675
Glu Gly Asp Gly	Ala Glu Asp Pro Thr	Val Gln Glu Ser Leu Val
680	685	690
Ser Glu Glu Ile	Val His Asp Leu Asp	Thr Cys Glu Val Thr Val
695	700	705
Glu Gly Glu Glu	Leu Asn His Glu Gln	Glu Ser Leu Glu Val Asp
710	715	720
Met Ala Arg Leu	Gln Gln Lys Gly Ile	Glu Val Ser Ser Ser Glu
725	730	735
Leu Gly Met Thr	Phe Thr Gly Val Asp	Thr Met Ala Ser Tyr Glu
740	745	750
Glu Val Leu His	Leu Leu Arg Tyr Arg	Asn Trp His Ala Arg Ser
755	760	765
Leu Leu Asp Arg	Lys Phe Lys Leu Ile	Cys Ser Glu Leu Asn Gly
770	775	780
Arg Tyr Ile Ser	Asn Glu Phe Lys Val	Glu Val Asn Val Ile His
785	790	795
Thr Ala Asn Pro	Met Glu His Ala Asn	His Met Ala Ala Gln Pro
800	805	810
Gln Phe Val His	Pro Glu His Arg Ser	Phe Val Asp Leu Ser Gly
815	820	825
His Asn Leu Ala	Asn Pro His Pro Phe	Ala Val Val Pro Ser Thr
830	835	840
Ala Thr Val Val	Ile Val Val Cys Val	Ser Phe Leu Val Phe Met
845	850	855
Ile Ile Leu Gly	Val Phe Arg Ile Arg	Ala Ala His Arg Arg Thr
860	865	870
Met Arg Asp Gln	Asp Thr Gly Lys Glu	Asn Glu Met Asp Trp Asp
875	880	885
Asp Ser Ala Leu	Thr Ile Thr Val Asn	Pro Met Glu Thr Tyr Glu
890	895	900
Asp Gln His Ser	Ser Glu Glu Glu Glu	Glu Glu Glu Glu Glu Glu
905	910	915
Glu Ser Glu Asp	Gly Glu Glu Glu Asp	Asp Ile Thr Ser Ala Glu
920	925	930
Ser Glu Ser Ser	Glu Val Glu Glu Gly	Glu Gln Gly Asp Pro Gln
935	940	945
Asn Ala Thr Arg	Gln Gln Gln Leu Glu	Trp Asp Asp Ser Thr Leu
950	955	960
Ser Tyr		

<210> 12
 <211> 953
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7509488CD1

<400> 12
 Met Leu Arg Arg Pro Ala Pro Arg Ala Val Pro Pro Ala Ala Arg
 1 5 10 15
 Leu Leu Leu Ala Gly Leu Leu Cys Gly Gly Val Trp Ala Ala
 20 25 30
 Arg Val Asn Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly
 35 40 45
 Ile Val Thr Glu Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu
 50 55 60
 Ile Ala Leu Asp Lys Asp Ala Pro Leu Arg Phe Ala Gly Glu Ile
 65 70 75
 Cys Gly Phe Lys Ile His Gly Gln Asn Val Pro Phe Asp Ala Val
 80 85 90
 Val Val Asp Lys Ser Thr Gly Glu Gly Val Ile Arg Ser Lys Glu
 95 100 105
 Lys Leu Asp Cys Glu Leu Gln Lys Asp Tyr Ser Phe Thr Ile Gln
 110 115 120
 Ala Tyr Asp Cys Gly Lys Gly Pro Asp Gly Thr Asn Val Lys Lys
 125 130 135
 Ser His Lys Ala Thr Val His Ile Gln Val Asn Asp Val Asn Glu
 140 145 150
 Tyr Ala Pro Val Phe Lys Glu Lys Ser Tyr Lys Ala Thr Val Ile
 155 160 165
 Glu Gly Lys Gln Tyr Asp Ser Ile Leu Arg Val Glu Ala Val Asp
 170 175 180
 Ala Asp Cys Ser Pro Gln Phe Ser Gln Ile Cys Ser Tyr Glu Ile
 185 190 195
 Ile Thr Pro Asp Val Pro Phe Thr Val Asp Lys Asp Gly Tyr Ile
 200 205 210
 Lys Asn Thr Glu Lys Leu Asn Tyr Gly Lys Glu His Gln Tyr Lys
 215 220 225
 Leu Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala Thr Glu
 230 235 240
 Asp Val Leu Val Lys Ile Ser Ile Lys Pro Thr Cys Thr Pro Gly
 245 250 255
 Trp Gln Gly Trp Asn Asn Arg Ile Glu Tyr Glu Pro Gly Thr Gly
 260 265 270
 Ala Leu Ala Val Phe Pro Asn Ile His Leu Glu Thr Cys Asp Glu
 275 280 285
 Pro Val Ala Ser Val Gln Ala Thr Val Glu Leu Glu Thr Ser His
 290 295 300
 Ile Gly Lys Gly Cys Asp Arg Asp Thr Tyr Ser Glu Lys Ser Leu
 305 310 315
 His Arg Leu Cys Gly Ala Ala Ala Gly Thr Ala Glu Leu Leu Pro
 320 325 330

Ser Pro Ser Gly	Ser Leu Asn Trp Thr	Met Gly Leu Pro Thr	Asp
335		340	345
Asn Gly His Asp	Ser Asp Gln Val Phe	Glu Phe Asn Gly Thr	Gln
350		355	360
Ala Val Arg Ile	Pro Asp Gly Val Val	Ser Val Ser Pro Lys	Glu
365		370	375
Pro Phe Thr Ile	Ser Val Trp Met Arg	His Gly Pro Phe Gly	Arg
380		385	390
Lys Lys Glu Thr	Ile Leu Cys Ser Ser	Asp Lys Thr Asp Met	Asn
395		400	405
Arg His His Tyr	Ser Leu Tyr Val His	Gly Cys Arg Leu Ile	Phe
410		415	420
Leu Phe Arg Gln	Asp Pro Ser Glu Glu	Lys Lys Tyr Arg Pro	Ala
425		430	435
Glu Phe His Trp	Lys Leu Asn Gln Val	Cys Asp Glu Glu Trp	His
440		445	450
His Tyr Val Leu	Asn Val Glu Phe Pro	Ser Val Thr Leu Tyr	Val
455		460	465
Asp Gly Thr Ser	His Glu Pro Phe Ser	Val Thr Glu Asp Tyr	Pro
470		475	480
Leu His Pro Ser	Lys Ile Glu Thr Gln	Leu Val Val Gly Ala	Cys
485		490	495
Trp Gln Gly Gly	Asp Leu His Met Thr	Gln Phe Phe Arg Gly	Asn
500		505	510
Leu Ala Gly Leu	Thr Leu Arg Ser Gly	Lys Leu Ala Asp Lys	Lys
515		520	525
Val Ile Asp Cys	Leu Tyr Thr Cys Lys	Glu Gly Leu Asp Leu	Gln
530		535	540
Val Leu Glu Asp	Ser Gly Arg Gly Val	Gln Ile Gln Ala His	Pro
545		550	555
Ser Gln Leu Val	Leu Thr Leu Glu Gly	Glu Asp Leu Gly Glu	Leu
560		565	570
Asp Lys Ala Met	Gln His Ile Ser Tyr	Leu Asn Ser Arg Gln	Phe
575		580	585
Pro Thr Pro Gly	Ile Arg Arg Leu Lys	Ile Thr Ser Thr Ile	Lys
590		595	600
Cys Phe Asn Glu	Ala Thr Cys Ile Ser	Val Pro Pro Val Asp	Gly
605		610	615
Tyr Val Met Val	Leu Gln Pro Glu Glu	Pro Lys Ile Ser Leu	Ser
620		625	630
Gly Val His His	Phe Ala Arg Ala Ala	Ser Glu Phe Glu Ser	Ser
635		640	645
Glu Gly Val Phe	Leu Phe Pro Glu Leu	Arg Ile Ile Ser Thr	Ile
650		655	660
Thr Arg Glu Val	Glu Pro Glu Gly Asp	Gly Ala Glu Asp Pro	Thr
665		670	675
Val Gln Glu Ser	Leu Val Ser Glu Glu	Ile Val His Asp Leu	Asp
680		685	690
Thr Cys Glu Val	Thr Val Glu Gly Glu	Glu Leu Asn His Glu	Gln
695		700	705
Glu Ser Leu Glu	Val Asp Met Ala Arg	Leu Gln Gln Lys Gly	Ile
710		715	720
Glu Val Ser Ser	Ser Glu Leu Gly Met	Thr Phe Thr Gly Val	Asp
725		730	735
Thr Met Ala Ser	Tyr Glu Glu Val Leu	His Leu Leu Arg Tyr	Arg
740		745	750

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Asn Trp His Ala Arg Ser Leu Leu Asp Arg Lys Phe Lys Leu Ile
    755                      760                      765
Cys Ser Glu Leu Asn Gly Arg Tyr Ile Ser Asn Glu Phe Lys Val
    770                      775                      780
Glu Val Asn Val Ile His Thr Ala Asn Pro Met Glu His Ala Asn
    785                      790                      795
His Met Ala Ala Gln Pro Gln Phe Val His Pro Glu His Arg Ser
    800                      805                      810
Phe Val Asp Leu Ser Gly His Asn Leu Ala Asn Pro His Pro Phe
    815                      820                      825
Ala Val Val Pro Ser Thr Ala Thr Val Val Ile Val Val Cys Val
    830                      835                      840
Ser Phe Leu Val Phe Met Ile Ile Leu Gly Val Phe Arg Ile Arg
    845                      850                      855
Ala Ala His Arg Arg Thr Met Arg Asp Gln Asp Thr Gly Lys Glu
    860                      865                      870
Asn Glu Met Asp Trp Asp Asp Ser Ala Leu Thr Ile Thr Val Asn
    875                      880                      885
Pro Met Glu Thr Tyr Glu Asp Gln His Ser Ser Glu Glu Glu Glu
    890                      895                      900
Glu Glu Glu Glu Glu Glu Glu Ser Glu Asp Gly Glu Glu Glu Asp
    905                      910                      915
Asp Ile Thr Ser Ala Glu Ser Glu Ser Ser Glu Val Glu Glu Gly
    920                      925                      930
Glu Gln Gly Asp Pro Gln Asn Ala Thr Arg Gln Gln Gln Leu Glu
    935                      940                      945
Trp Asp Asp Ser Thr Leu Ser Tyr
    950

```

<210> 13

<211> 582

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510060CD1

<400> 13

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Met Ile Phe Leu Thr Ala Leu Pro Leu Phe Trp Ile Met Ile Ser
    1                      5                      10                      15
Ala Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile
    20                      25                      30
Ser Ala Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp
    35                      40                      45
Phe Pro Asp Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr
    50                      55                      60
Phe Asn Ser Pro Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys
    65                      70                      75
Ser Arg Thr Gln Val Val His Glu Ser Phe Gln Gly Arg Ser Arg
    80                      85                      90
Leu Leu Gly Asp Glu Gly Leu Arg Asn Cys Thr Leu Leu Leu Ser
    95                      100                     105
Asn Val Ser Pro Glu Leu Gly Gly Lys Tyr Tyr Phe Arg Gly Asp
    110                     115                     120
Leu Gly Gly Tyr Asn Gln Tyr Thr Phe Ser Glu His Ser Val Leu

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	125		130		135
Asp Ile Val Asn Thr Pro Asn Ile Val Val Pro Pro Glu Val Val					
	140		145		150
Ala Gly Thr Glu Val Glu Val Ser Cys Met Val Pro Asp Asn Cys					
	155		160		165
Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly His Glu Gly Leu					
	170		175		180
Gly Glu Pro Ala Val Leu Gly Arg Leu Arg Glu Asp Glu Gly Thr					
	185		190		195
Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg Glu Ala					
	200		205		210
Asn Gly His Arg Leu Gly Cys Gln Ala Ser Phe Pro Asn Thr Thr					
	215		220		225
Leu Gln Phe Glu Gly Tyr Ala Ser Met Asp Val Lys Tyr Pro Pro					
	230		235		240
Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser					
	245		250		255
His Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu					
	260		265		270
Leu Thr Trp Met Arg Asp Gly Thr Val Leu Arg Glu Ala Val Ala					
	275		280		285
Glu Ser Leu Leu Leu Glu Leu Glu Glu Val Thr Pro Ala Glu Asp					
	290		295		300
Gly Val Tyr Ala Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn					
	305		310		315
Arg Thr Val Gly Leu Ser Val Met Tyr Ala Pro Trp Lys Pro Thr					
	320		325		330
Val Asn Gly Thr Met Val Ala Val Glu Gly Glu Thr Val Ser Ile					
	335		340		345
Leu Cys Ser Thr Gln Ser Asn Pro Asp Pro Ile Leu Thr Ile Phe					
	350		355		360
Lys Glu Lys Gln Ile Leu Ser Thr Val Ile Tyr Glu Ser Glu Leu					
	365		370		375
Gln Leu Glu Leu Pro Ala Val Ser Pro Glu Asp Asp Gly Glu Tyr					
	380		385		390
Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln Arg Ala Thr Ala Phe					
	395		400		405
Asn Leu Ser Val Glu Phe Ala Pro Val Leu Leu Leu Glu Ser His					
	410		415		420
Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys Val Val Lys					
	425		430		435
Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser Arg Asn					
	440		445		450
Val Thr Val Asn Glu Ser Glu Arg Glu Phe Val Tyr Ser Glu Arg					
	455		460		465
Ser Gly Leu Val Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala					
	470		475		480
Gln Ala Pro Pro Arg Val Ile Cys Thr Ala Arg Asn Leu Tyr Gly					
	485		490		495
Ala Lys Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg Leu Met					
	500		505		510
Trp Ala Lys Ile Gly Pro Val Gly Ala Val Val Ala Phe Ala Ile					
	515		520		525
Leu Ile Ala Ile Val Cys Tyr Ile Thr Gln Thr Arg Arg Lys Lys					
	530		535		540
Asn Val Thr Glu Ser Pro Ser Phe Ser Ala Gly Asp Asn Pro Pro					

	20		25		30
Leu Arg Leu Ser Phe Gln Glu Leu Gln Ala Trp His Gly Leu Gln					
	35		40		45
Thr Phe Ser Leu Glu Arg Thr Cys Cys Tyr Gln Ala Leu Leu Val					
	50		55		60
Asp Glu Glu Arg Gly Arg Leu Phe Val Gly Ala Glu Asn His Val					
	65		70		75
Ala Ser Leu Asn Leu Asp Asn Ile Ser Lys Arg Ala Lys Lys Leu					
	80		85		90
Ala Trp Pro Ala Pro Val Glu Trp Arg Glu Glu Cys Asn Trp Ala					
	95		100		105
Gly Lys Asp Ile Gly Thr Glu Cys Met Asn Phe Val Lys Leu Leu					
	110		115		120
His Ala Tyr Asn Arg Thr His Leu Leu Ala Cys Gly Thr Gly Ala					
	125		130		135
Phe His Pro Thr Cys Ala Phe Val Glu Val Gly His Arg Ala Glu					
	140		145		150
Glu Pro Val Leu Arg Leu Asp Pro Gly Arg Ile Glu Asp Gly Lys					
	155		160		165
Gly Lys Ser Pro Tyr Asp Pro Arg His Arg Ala Ala Ser Val Leu					
	170		175		180
Val Gly Glu Glu Leu Tyr Ser Gly Val Ala Ala Asp Leu Met Gly					
	185		190		195
Arg Asp Phe Thr Ile Phe Arg Ser Leu Gly Gln Arg Pro Ser Leu					
	200		205		210
Arg Thr Glu Pro His Asp Ser Arg Trp Leu Asn Glu Pro Lys Phe					
	215		220		225
Val Lys Val Phe Trp Ile Pro Glu Ser Glu Asn Pro Asp Asp Asp					
	230		235		240
Lys Ile Tyr Phe Phe Phe Arg Glu Thr Ala Val Glu Ala Ala Pro					
	245		250		255
Ala Leu Gly Arg Leu Ser Val Ser Arg Val Gly Gln Ile Cys Arg					
	260		265		270
Asn Asp Val Gly Gly Gln Arg Ser Leu Val Asn Lys Trp Thr Thr					
	275		280		285
Phe Leu Lys Ala Arg Leu Val Cys Ser Val Pro Gly Val Glu Gly					
	290		295		300
Asp Thr His Phe Asp Gln Leu Arg Glu Cys Gly Ser Gly Tyr Gly					
	305		310		315
Val Gly Glu Gly Gly Ser Gly Ala Asp Ser Gly Ser Pro Arg Arg					
	320		325		330
Ser Gly Ala Val Arg Pro Thr Pro Ala Arg Pro Leu Pro Arg Arg					
	335		340		345
Gly Cys Val Ser Val Val Leu Ala Gly Pro Pro Asp Pro Ala Ala					
	350		355		360
Leu Cys Arg Leu Leu His Val Gln Gln His Leu Pro Gly Leu Cys					
	365		370		375
Gly Val Arg Val Gln His Glu Arg Arg Ala Pro Gly Leu Leu Gly					
	380		385		390
Thr Leu Cys Thr Gln Gly Gly Ala His Ala Pro Val Gly Val Ile					
	395		400		405
Pro Gly Ser Arg Pro Leu Pro Ala Ala Arg His Val Pro Gln Gln					
	410		415		420
Asp Leu Trp His Leu Gln Phe His Gln Gly Leu Pro Arg Arg Cys					
	425		430		435
His Pro Val Cys Ala Glu Pro Pro Pro His Val Gln Leu Cys Pro					

	440		445		450
Ala His Trp Gly	Ala Pro Ser Phe Pro Thr Ser Trp Ser Gln Leu				
	455		460		465
His Leu His Ser Asn Cys Arg Gly Pro Gly Cys Ser Arg					
	470		475		

<210> 16

<211> 412

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7511618CD1

<400> 16

Met Ala Glu Ser Gly Glu Ser Gly Gly Pro Pro Gly Ser Gln Asp		
1	5	10 15
Ser Ala Ala Gly Ala Glu Gly Ala Gly Ala Pro Ala Ala Ala Ala		
	20	25 30
Ser Ala Glu Pro Lys Ile Met Lys Val Thr Val Lys Thr Pro Lys		
	35	40 45
Glu Lys Glu Glu Phe Ala Val Pro Glu Asn Ser Ser Val Gln Gln		
	50	55 60
Thr Leu Glu Leu Ala Arg Asn Pro Ala Met Met Gln Glu Met Met		
	65	70 75
Arg Asn Gln Asp Arg Ala Leu Ser Asn Leu Glu Ser Ile Pro Gly		
	80	85 90
Gly Tyr Asn Ala Leu Arg Arg Met Tyr Thr Asp Ile Gln Glu Pro		
	95	100 105
Met Leu Ser Ala Ala Gln Glu Gln Phe Gly Gly Asn Pro Phe Ala		
	110	115 120
Ser Leu Val Ser Asn Thr Ser Ser Gly Glu Gly Ser Gln Pro Ser		
	125	130 135
Arg Thr Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala Pro Gln		
	140	145 150
Thr Ser Gln Ser Ser Ser Ala Ser Ser Gly Thr Ala Ser Thr Val		
	155	160 165
Gly Gly Thr Thr Gly Ser Thr Ala Ser Gly Thr Ser Gly Gln Ser		
	170	175 180
Thr Thr Ala Pro Asn Leu Val Pro Gly Val Gly Ala Ser Met Phe		
	185	190 195
Asn Thr Pro Gly Met Gln Ser Leu Leu Gln Gln Ile Thr Glu Asn		
	200	205 210
Pro Gln Leu Met Gln Asn Met Leu Ser Ala Pro Tyr Met Arg Ser		
	215	220 225
Met Met Gln Ser Leu Ser Gln Asn Pro Asp Leu Ala Ala Gln Met		
	230	235 240
Met Leu Asn Asn Pro Leu Phe Ala Gly Asn Pro Gln Leu Gln Glu		
	245	250 255
Gln Met Arg Gln Gln Leu Pro Thr Phe Leu Gln Gln Met Gln Asn		
	260	265 270
Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala Met Gln Ala		
	275	280 285
Leu Leu Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr Glu Ala		
	290	295 300

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Pro Gly Leu Ile Pro Gly Phe Thr Pro Gly Leu Gly Ala Leu Gly
      305              310              315
Ser Thr Gly Gly Ser Ser Gly Thr Asn Gly Ser Asn Ala Thr Pro
      320              325              330
Ser Glu Asn Thr Ser Pro Thr Ala Gly Thr Thr Glu Pro Gly His
      335              340              345
Gln Gln Phe Ile Gln Gln Met Leu Gln Ala Leu Ala Gly Val Asn
      350              355              360
Pro Gln Leu Gln Asn Pro Glu Val Arg Phe Gln Gln Gln Leu Glu
      365              370              375
Gln Leu Ser Ala Met Gly Phe Leu Asn Arg Glu Ala Asn Leu Gln
      380              385              390
Ala Leu Ile Ala Thr Gly Gly Asp Ile Asn Ala Ala Ile Glu Arg
      395              400              405
Leu Leu Gly Ser Gln Pro Ser
      410

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<210> 17

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 6244135CD1

<400> 17

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Met Met Asp Gln Glu Glu Lys Thr Glu Glu Gly Ser Gly Pro Cys
  1              5              10              15
Ala Glu Ala Gly Ser Pro Asp Gln Glu Gly Phe Phe Asn Leu Leu
      20              25              30
Ser His Val Gln Gly Asp Arg Met Glu Gly Gln Arg Cys Ser Leu
      35              40              45
Gln Ala Gly Pro Gly Gln Thr Thr Lys Ser Gln Ser Asp Pro Thr
      50              55              60
Pro Glu Met Asp Ser Leu Met Asp Met Leu Ala Ser Thr Gln Gly
      65              70              75
Arg Arg Met Asp Asp Gln Arg Val Thr Val Ser Ser Leu Pro Gly
      80              85              90
Phe Gln Pro Val Gly Ser Lys Asp Gly Ala Gln Lys Arg Ala Gly
      95              100             105
Thr Leu Ser Pro Gln Pro Leu Leu Thr Pro Gln Asp Pro Thr Ala
      110             115             120
Leu Gly Phe Arg Arg Asn Ser Ser Pro Gln Pro Pro Thr Gln Ala
      125             130             135
Pro

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<210> 18

<211> 198

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506689CD1

<400> 18

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Met Pro Ala Ser Ala Ala Arg Pro Arg Pro Gly Pro Gly Gln Pro
 1              5              10              15
Thr Ala Ser Pro Phe Pro Leu Leu Leu Leu Ala Val Leu Ser Gly
      20              25              30
Pro Val Ser Gly Arg Val Pro Arg Ser Val Pro Arg Thr Ser Leu
      35              40              45
Pro Ile Ser Glu Ala Asp Ser Cys Leu Thr Arg Phe Ala Val Pro
      50              55              60
His Thr Tyr Asn Tyr Ser Val Leu Leu Val Asp Pro Ala Ser His
      65              70              75
Thr Leu Tyr Val Gly Ala Arg Asp Thr Ile Phe Ala Leu Ser Leu
      80              85              90
Pro Phe Ser Gly Glu Arg Pro Arg Arg Ile Asp Trp Met Val Pro
      95              100             105
Glu Ala His Arg Gln Asn Cys Arg Lys Lys Gly Lys Lys Glu Gly
      110             115             120
Asp Leu Gly Gly Arg Lys Thr Leu Gln Gln Arg Trp Thr Thr Phe
      125             130             135
Leu Lys Ala Asp Leu Leu Cys Pro Gly Leu Ser Met Ala Gly Pro
      140             145             150
Pro Val Ser Cys Arg Met Leu Leu Cys Phe Asp Leu Ser Leu Gly
      155             160             165
Gln Gly Leu Pro Ser Phe Met Ala Ser Phe Leu Pro Ser Gly Arg
      170             175             180
Gly Leu Leu Ser Leu Leu Ser Val Pro Ser Asp His Lys Thr Phe
      185             190             195
Gly Gln Cys

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<210> 19

<211> 813

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510185CD1

<400> 19

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Met Ala Val Gln Arg Ala Ala Ser Pro Arg Arg Pro Pro Ala Pro
 1              5              10              15
Leu Trp Pro Arg Leu Leu Leu Pro Leu Leu Leu Leu Leu Pro
      20              25              30
Ala Pro Ser Glu Gly Leu Gly His Ser Ala Glu Leu Ala Phe Ala
      35              40              45
Val Glu Pro Ser Asp Asp Val Ala Val Pro Gly Gln Pro Ile Val
      50              55              60
Leu Asp Cys Arg Val Glu Gly Thr Pro Pro Val Arg Ile Thr Trp
      65              70              75
Arg Lys Asn Gly Val Glu Leu Pro Glu Ser Thr His Ser Thr Leu
      80              85              90
Leu Ala Asn Gly Ser Leu Met Ile Arg His Phe Arg Leu Glu Pro
      95              100             105
Gly Gly Ser Pro Ser Asp Glu Gly Asp Tyr Glu Cys Val Ala Gln
      110             115             120

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Asn Arg Phe Gly Leu Val Val Ser Arg Lys Ala Arg Ile Gln Ala	125	130	135
Ala Thr Met Ser Asp Phe His Val His Pro Gln Ala Thr Val Gly	140	145	150
Glu Glu Gly Gly Val Ala Arg Phe Gln Cys Gln Ile His Gly Leu	155	160	165
Pro Lys Pro Leu Ile Thr Trp Glu Lys Asn Arg Val Pro Ile Asp	170	175	180
Thr Asp Asn Glu Arg Tyr Thr Leu Leu Pro Lys Gly Val Leu Gln	185	190	195
Ile Thr Gly Leu Arg Ala Glu Asp Gly Gly Ile Phe His Cys Val	200	205	210
Ala Ser Asn Ile Ala Ser Ile Arg Ile Ser His Gly Ala Arg Leu	215	220	225
Thr Val Ser Gly Ser Gly Ser Gly Ala Tyr Lys Glu Pro Ala Ile	230	235	240
Leu Val Gly Pro Glu Asn Leu Thr Leu Thr Val His Gln Thr Ala	245	250	255
Val Leu Glu Cys Val Ala Thr Gly Asn Pro Arg Pro Ile Val Ser	260	265	270
Trp Ser Arg Leu Asp Gly Arg Pro Ile Gly Val Glu Gly Ile Gln	275	280	285
Val Leu Gly Thr Gly Asn Leu Ile Ile Ser Asp Val Thr Val Gln	290	295	300
His Ser Gly Val Tyr Val Cys Ala Ala Asn Arg Pro Gly Thr Arg	305	310	315
Val Arg Arg Thr Ala Gln Gly Arg Leu Val Val Gln Ala Pro Ala	320	325	330
Glu Phe Val Gln His Pro Gln Ser Ile Ser Arg Pro Ala Gly Thr	335	340	345
Thr Ala Met Phe Thr Cys Gln Ala Gln Gly Glu Pro Pro Pro His	350	355	360
Val Thr Trp Leu Lys Asn Gly Gln Val Leu Gly Pro Gly Gly His	365	370	375
Val Arg Leu Lys Asn Asn Asn Ser Thr Leu Thr Ile Ser Gly Ile	380	385	390
Gly Pro Glu Asp Glu Ala Ile Tyr Gln Cys Val Ala Glu Asn Ser	395	400	405
Ala Gly Ser Ser Gln Ala Ser Ala Arg Leu Thr Val Leu Trp Ala	410	415	420
Glu Gly Leu Pro Gly Pro Pro Arg Asn Val Arg Ala Val Ser Val	425	430	435
Ser Ser Thr Glu Val Arg Val Ser Trp Ser Glu Pro Leu Ala Asn	440	445	450
Thr Lys Glu Ile Ile Gly Tyr Val Leu His Ile Arg Lys Ala Ala	455	460	465
Asp Pro Pro Glu Leu Glu Tyr Gln Glu Ala Val Ser Lys Ser Thr	470	475	480
Phe Gln His Leu Val Ser Asp Leu Glu Pro Ser Thr Ala Tyr Ser	485	490	495
Phe Tyr Ile Lys Ala Tyr Thr Pro Arg Gly Ala Ser Ser Ala Ser	500	505	510
Val Pro Thr Leu Ala Ser Thr Leu Gly Glu Ala Pro Ala Pro Pro	515	520	525
Pro Leu Ser Val Arg Val Leu Gly Ser Ser Ser Leu Gln Leu Leu	530	535	540

Trp Glu Pro Trp Pro Arg Leu Ala Gln His Glu Gly Gly Phe Lys
 545 550 555
 Leu Phe Tyr Arg Pro Ala Ser Lys Thr Ser Phe Thr Gly Pro Ile
 560 565 570
 Leu Leu Pro Gly Thr Val Ser Ser Tyr Asn Leu Ser Gln Leu Asp
 575 580 585
 Pro Thr Ala Val Tyr Glu Val Lys Leu Leu Ala Tyr Asn Gln His
 590 595 600
 Gly Asp Gly Asn Ala Thr Val Arg Phe Val Ser Leu Arg Gly Ala
 605 610 615
 Ser Glu Arg Thr Ala Leu Ser Pro Pro Cys Asp Cys Arg Lys Glu
 620 625 630
 Glu Ala Ala Asn Gln Thr Ser Thr Thr Gly Ile Val Ile Gly Ile
 635 640 645
 His Ile Gly Val Thr Cys Ile Ile Phe Cys Val Leu Phe Leu Leu
 650 655 660
 Phe Gly Gln Arg Gly Arg Val Leu Leu Cys Lys Asp Val Glu Asn
 665 670 675
 Gln Leu Ser Pro Pro Gln Gly Pro Arg Ser Gln Arg Asp Pro Gly
 680 685 690
 Ile Leu Ala Leu Asn Gly Ala Arg Arg Gly Gln Arg Gly Gln Leu
 695 700 705
 Gly Arg Asp Glu Lys Arg Val Asp Met Lys Glu Leu Glu Gln Leu
 710 715 720
 Phe Pro Pro Ala Ser Ala Ala Gly Gln Pro Asp Pro Arg Pro Thr
 725 730 735
 Asp Pro Ala Ala Pro Ala Pro Cys Glu Glu Thr Gln Leu Ser Leu
 740 745 750
 Leu Pro Leu Gln Gly Cys Gly Leu Met Glu Gly Lys Thr Thr Glu
 755 760 765
 Ala Lys Thr Thr Glu Ala Thr Ala Pro Cys Ala Gly Leu Ala Ala
 770 775 780
 Ala Pro Pro Pro Pro Asp Gly Gly Pro Gly Leu Leu Ser Glu Gly
 785 790 795
 Gln Ala Ser Arg Pro Ala Ala Ala Arg Val Thr Gln Pro Ala His
 800 805 810
 Ser Glu Gln

<210> 20

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1420867CD1

<400> 20

Met Trp Ile Asp Ile Phe Pro Gln Asp Val Pro Ala Pro Pro Pro
 1 5 10 15
 Val Asp Ile Lys Pro Arg Gln Pro Ile Ser Tyr Glu Leu Arg Val
 20 25 30
 Val Ile Trp Asn Thr Glu Asp Val Val Leu Asp Asp Glu Asn Pro
 35 40 45
 Leu Thr Gly Glu Met Ser Ser Asp Ile Tyr Val Lys Ser Trp Val

	50		55		60
Lys Gly Leu Glu His Asp Lys Gln Glu Thr Asp Val His Phe Asn					
	65		70		75
Ser Leu Thr Gly Glu Gly Asn Phe Asn Trp Arg Phe Val Phe Arg					
	80		85		90
Phe Asp Tyr Leu Pro Thr Glu Arg Glu Val Ser Val Arg Arg Arg					
	95		100		105
Ser Gly Pro Phe Ala Leu Glu Glu Ala Glu Phe Arg Gln Pro Ala					
	110		115		120
Val Leu Val Leu Gln Asp Pro Trp Ser Cys Ser Tyr Gln Thr Trp					
	125		130		135
Cys Met Gly Pro Gly Ala Pro Ser Ser Ala Leu Cys Ser Trp Pro					
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Ala Met Gly Pro Gly Arg Gly Ala Ile Cys Phe Ala Ala Ala Ala					
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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7512289CD1

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Pro Asp Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val					
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Pro Val Gly Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly					
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Leu Ala Phe Met Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu					
	65		70		75
Tyr Lys Tyr Phe Ala Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly					
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Ile Lys Tyr Ile Lys Asp Asp Val Ile Leu Asn Glu Pro Ser Ala					
	95		100		105
Asp Ala Pro Ala Ala Leu Tyr Gln Thr Ile Glu Glu Asn Ile Lys					
	110		115		120
Ile Phe Glu Glu Glu Glu Val Glu Phe Ile Ser Val Pro Val Pro					
	125		130		135
Glu Phe Ala Asp Ser Asp Pro Ala Asn Ile Val His Asp Phe Asn					
	140		145		150
Lys Ala Gly Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His					
	155		160		165
Met Val Ile Thr Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe					
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Phe Ile Tyr Arg Leu Cys His Asp Lys Glu Thr Tyr Lys Leu Gln					
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Arg Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn					
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Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr					

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Tyr	Leu	Thr	Val	Leu	Cys	Met	Pro	Gly	Val	Ile	Arg	Cys	Pro	Val	320	325	330
Arg	Ala	Asn	Pro	Pro	Leu	Leu	Phe	Val	Ser	Trp	Thr	Lys	Asp	Gly	335	340	345
Lys	Ala	Leu	Gln	Leu	Asp	Lys	Phe	Pro	Gly	Trp	Ser	Gln	Gly	Thr	350	355	360
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Leu	Ile	Pro	Cys	Ser	Ala	Gln	Gly	Asp	Pro	Pro	Pro	Val	Val	Ser	425	430	435
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Pro	Ser	Arg	Thr	Gln	Leu	Pro	Gly	Leu	Leu	Pro	Gln	Pro	Val	Leu	710	715	720
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Ser Ser Ser Ser Pro Ser Gly Ala Pro Gln Pro Leu Cys Ile Glu	875	880	885
Asp Ile Ser Pro Val Ala Pro Pro Pro Ala Ala Pro Pro Ser Pro	890	895	900
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Phe Arg Glu Met Asn Val Asp Gly Asp Trp Pro Pro Leu Glu Glu	920	925	930
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Arg Leu Leu Pro Gly Leu Leu Pro Ala Ala Pro Arg Gly Ser Leu	995	1000	1005
Thr Ser Gln Ser Ser Gly Arg Gly Ser Ala Ser Phe Leu Arg Pro	1010	1015	1020
Pro Ser Thr Ala Pro Ser Ala Gly Gly Ser Tyr Leu Ser Pro Ala	1025	1030	1035
Pro Gly Asp Thr Ser Ser Trp Ala Ser Gly Pro Glu Arg Trp Pro	1040	1045	1050
Arg Arg Glu His Val Val Thr Val Ser Lys Arg Arg Asn Thr Ser	1055	1060	1065
Val Asp Glu Asn Tyr Glu Trp Asp Ser Glu Phe Pro Gly Asp Met	1070	1075	1080
Glu Leu Leu Glu Thr Leu His Leu Gly Leu Ala Ser Ser Arg Leu	1085	1090	1095
Arg Pro Glu Ala Glu Pro Glu Leu Gly Val Lys Thr Pro Glu Glu	1100	1105	1110
Gly Cys Leu Leu Asn Thr Ala His Val Thr Gly Pro Glu Ala Arg	1115	1120	1125
Cys Ala Ala Leu Arg Glu Glu Phe Leu Ala Phe Arg Arg Arg Arg	1130	1135	1140
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His Pro Glu Gln Ala Thr Leu Leu
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<213> Homo sapiens

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<211> 2259

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 7503554CB1

<400> 25

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<211> 1522

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506077CB1

<400> 26

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<210> 27

<211> 1099

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506765CB1

<400> 27

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<210> 28

<211> 3311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7490048CB1

<400> 28

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<211> 1874

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2133585CB1

<400> 29

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<210> 30

<211> 4211

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7509063CB1

<400> 30

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<213> Homo sapiens

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<220>

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<223> Incyte ID No: 7511618CB1

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<213> Homo sapiens

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<400> 39

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<211> 2660

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7506689CB1

<400> 40

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<211> 2761

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7510185CB1

<400> 41

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<211> 1440

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1420867CB1

<400> 42

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<210> 43

<211> 1066

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<223> Incyte ID No: 7512289CB1

<400> 43

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/40059

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/00, 15/85, 15/86; C07K 5/00, 14/00; A61K 38/00
 US CL : 435/69.1,325; 514/2; 530/300,350; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1,325; 514/2; 530/300,350; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2002/0155577 A1 (KOUTNIKOVA et al.) 24 October 2002 (24.10.2002), entire document.	1-7, 9-10, 12-13, 56, 69, 78, 91
A	WANG, X. Rim1 and Raphipilin-3 Bind Rab3-GTP by Composite Determinants Partially Related through N-terminal alpha-Helix Motifs. The Journal of Biological Chemistry 31 August 2001, Vol. 276, No. 35, pages 32480-32488, entire document.	1-7, 9-10, 12-13, 56, 69, 78, 91
A	STROM, M. A Family of Rab27-binding Proteins. The Journal of Biological Chemistry 12 July 2002, Vol. 277, No. 28, pages 25423-25430, entire document.	1-7, 9-10, 12-13, 56, 69, 78, 91
A	BURGOYNE, R.D. Control of Membrane Fusion Dynamics during Regulated Exocytosis. Biochemical Society Transactions August 2001, Vol. 29, No. 4, pages 467-472, entire document	1-7, 9-10, 12-13, 56, 69, 78, 91
A	FUKUDA et al. Novel Splicing Isoforms of Synaptotagmin-like Proteins 2 and 3: identification of the Slp Homology domain. Biochemical and Biophysical Research Communications 04 May 2001, Vol. 283, No. 2, pages 513-519, entire document.	1-7, 9-10, 12-13, 56, 69, 78, 91
X	WO 01/46256 A2 (INCYTE GENOMICS, INC.) 28 June 2001 (28.06.2001), pages 28-29 (SEQ ID NO: 26 shares 62.3% homology with SEQ ID NO: 23).	1-7, 9-10, 12-13, 56, 69, 78, 91



Further documents are listed in the continuation of Box C.



See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"B" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"Z" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

25 April 2003 (25.04.2003)

Date of mailing of the international search report

23 MAY 2003

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
 Box PCT
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Authorized officer

Christopher Nichols, Ph.D.

Telephone No. 703-308-0196

INTERNATIONAL SEARCH REPORT

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01/60857 A2 (AVENTIS PHARMA S.A.) 23 August 2001 (23.08.2001), Claim 10, Figure 9 (87.7% homology with SEQ ID NO: 1), Claim 10 pages 77-80 (87.7% homology with SEQ ID NO: 1); and pages 1-27 (SEQ ID NO: 1 shares 58.8% homology with SEQ ID NO: 23; SEQ ID NO: 12 shares 68.1% homology with SEQ ID NO: 23; SEQ ID NO: 14 shares 62.5% homology with SEQ ID NO: 23; SEQ ID NO: 42 shares 68.1% homology with SEQ ID NO: 23; SEQ ID NO: 44 shares 62.5% homology with SEQ ID NO: 23).	1-7, 9-10, 12-13, 56, 69, 78, 91
X	WO 01/75067 A2 (HYSEQ, INC.) 11 October 2001 (11.10.2001), claim 20, SEQ ID NO: 47280 (shares 71.1% homology with SEQ ID NO: 1), SEQ ID NO: 47279 (shares 77.9% homology with SEQ ID NO: 1).	1-7, 9-10, 12-13, 56, 69, 78, 91
X	WANG et al. Novel Rapphilin-3-like Protein Associates with Insulin-Containing Granules in Pancreatic Beta Cells. The Journal of Biological Chemistry 01 October 1999, Vol. 274, No. 40, pages 28543-28548 (Figure 1, 36.5% homology with SEQ ID NO: 1).	1-7, 9-10, 12-13, 56, 69, 78, 91
X	CASTETS et al. Zinedin, SG2NA, and Striatin Are Calmodulin-binding, WD Repeat Proteins Principally Expressed in the Brain. The Journal of Biological Chemistry 30 June 2000, Vol. 275, No. 26, pages 19970-19977 (Figure 1; 94.7% and 90.3% homology with SEQ ID NO: 14).	1-7, 9-10, 12-13, 56, 69, 78, 91
Y	HAYNES et al. A Direct Inhibitory Role for the Rab3-specific Effector, Noc2, in Ca ²⁺ -regulated Exocytosis in Neuroendocrine Cells. The Journal of Biological Chemistry, Vol. 276, No. 13, pages 9726-9732 (Figure 3).	1-7, 9-10, 12-13, 56, 69, 78, 91
Y	MATESIC et al. Mutations in Mlph, encoding a member of the Rab effector family, cause the melanosome transport defects observed in leaden mice. PNAS 28 August 2001, Vol. 98, No. 18, pages 10238-10243 (Figure 4).	1-7, 9-10, 12-13, 56, 69, 78, 91

INTERNATIONAL SEARCH REPORT

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group 1, claim(s) 1-7, 9-10, 12-13, 17-18, 56, and 78 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 1, an isolated polypeptide comprising SEQ ID NO: 1, an isolated polynucleotides comprising SEQ ID NO: 23, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 2, claim(s) 1-7, 9-10, 12-13, 17-18, 57, and 79 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 2, an isolated polypeptide comprising SEQ ID NO: 2, an isolated polynucleotides comprising SEQ ID NO: 24, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 3 claim(s) 1-7, 9-10, 12-13, 17-18, 58, and 80 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 3, an isolated polypeptide comprising SEQ ID NO: 3, an isolated polynucleotides comprising SEQ ID NO: 25, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 4 claim(s) 1-7, 9-10, 12-13, 17-18, 59, and 81 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 4, an isolated polypeptide comprising SEQ ID NO: 4, an isolated polynucleotides comprising SEQ ID NO: 26, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 5 claim(s) 1-7, 9-10, 12-13, 17-18, 60, and 82 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 5, an isolated polypeptide comprising SEQ ID NO: 5, an isolated polynucleotides comprising SEQ ID NO: 27, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 6 claim(s) 1-7, 9-10, 12-13, 17-18, 61, and 83 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 6, an isolated polypeptide comprising SEQ ID NO: 6, an isolated polynucleotides comprising SEQ ID NO: 28, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 7 claim(s) 1-7, 9-10, 12-13, 17-18, 62, and 84 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 7, an isolated polypeptide comprising SEQ ID NO: 7, an isolated polynucleotides comprising SEQ ID NO: 29, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 8 claim(s) 1-7, 9-10, 12-13, 17-18, 63, and 85 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 8, an isolated polypeptide comprising SEQ ID NO: 8, an isolated polynucleotides comprising SEQ ID NO: 30, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 9 claim(s) 1-7, 9-10, 12-13, 17-18, 64, and 86 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 9, an isolated polypeptide comprising SEQ ID NO: 9, an isolated polynucleotides comprising SEQ ID NO: 31, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 10 claim(s) 1-7, 9-10, 12-13, 17-18, 65, and 87 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 10, an isolated polypeptide comprising SEQ ID NO: 10, an isolated polynucleotides comprising SEQ ID NO: 32, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 11, claim(s) 1-7, 9-10, 12-13, 17-18, 66, and 88 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 11, an isolated polypeptide comprising SEQ ID NO: 11, an isolated polynucleotides comprising SEQ ID NO: 33, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 12, claim(s) 1-7, 9-10, 12-13, 17-18, 67, and 89 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 12, an isolated polypeptide comprising SEQ ID NO: 12, an isolated polynucleotides comprising SEQ ID NO: 34, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

INTERNATIONAL SEARCH REPORT

PCT/US02/40059

Group 13 claim(s) 1-7, 9-10, 12-13, 17-18, 68, and 90 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 13, an isolated polypeptide comprising SEQ ID NO: 13, an isolated polynucleotides comprising SEQ ID NO: 35, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 14 claim(s) 1-7, 9-10, 12-13, 17-18, 69, and 91 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 14, an isolated polypeptide comprising SEQ ID NO: 14, an isolated polynucleotides comprising SEQ ID NO: 36, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 15 claim(s) 1-7, 9-10, 12-13, 17-18, 70, and 92 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 15, an isolated polypeptide comprising SEQ ID NO: 15, an isolated polynucleotides comprising SEQ ID NO: 37, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 16 claim(s) 1-7, 9-10, 12-13, 17-18, 71, and 93 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 16, an isolated polypeptide comprising SEQ ID NO: 16, an isolated polynucleotides comprising SEQ ID NO: 38, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 17 claim(s) 1-7, 9-10, 12-13, 17-18, 72, and 94 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 17, an isolated polypeptide comprising SEQ ID NO: 17, an isolated polynucleotides comprising SEQ ID NO: 39, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 18 claim(s) 1-7, 9-10, 12-13, 17-18, 73 and 95 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 18, an isolated polypeptide comprising SEQ ID NO: 18, an isolated polynucleotides comprising SEQ ID NO: 40, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 19 claim(s) 1-7, 9-10, 12-13, 17-18, 74, and 96 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 19, an isolated polypeptide comprising SEQ ID NO: 19, an isolated polynucleotides comprising SEQ ID NO: 41, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 20 claim(s) 1-7, 9-10, 12-13, 17-18, 75 and 97 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 20, an isolated polypeptide comprising SEQ ID NO: 20, an isolated polynucleotides comprising SEQ ID NO: 42, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 21, claim(s) 1-7, 9-10, 12-13, 17-18, 76, and 98 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 21, an isolated polypeptide comprising SEQ ID NO: 21, an isolated polynucleotides comprising SEQ ID NO: 43, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 22, claim(s) 1-7, 9-10, 12-13, 17-18, 77, and 99 (each in part), drawn to a method of producing a polypeptide comprising SEQ ID NO: 22, an isolated polypeptide comprising SEQ ID NO: 22, an isolated polynucleotides comprising SEQ ID NO: 44, cells transformed with said polynucleotides, promoter sequences, and compositions comprising same.

Group 23 claim(s) 8, drawn to a transgenic organism.

Group 24 claim(s) 11, 31, 32, 34, and 36-43 drawn to a method of preparing an antibody, polyclonal and monoclonal antibodies, and compositions comprising same.

Group 25 claim(s) 14-16, drawn to a method of detecting a target polynucleotides in a sample.

Group 26 claim(s) 19 and 22, drawn to a method for treating a disease or condition associated with *decreased* expression of functional NTRN.

Group 27 claim(s) 20 and 21, drawn to a method of screening for effectiveness as an *agonist* of a polypeptide and compositions comprising same.

Group 28 claim(s) 23 and 24, drawn to drawn to a method of screening for effectiveness as an *antagonist* of a polypeptide and compositions comprising same.

Group 29 claim(s) 25, drawn to drawn to a method for treating a disease or condition associated with *overexpression* of functional NTRN.

Group 30 claim(s) 26, drawn to a method of screening for a compound that specifically binds to a polypeptide.

INTERNATIONAL SEARCH REPORT

PCT/US02/40059

Group 31, claim(s) 27, drawn to a method of screening for a compound that modulates the activity of a polypeptide.

Group 32, claim(s) 28, drawn to a method of screening a compound for effectiveness in altering expression of a target polynucleotide.

Group 33 claim(s) 29, drawn to a method of assessing toxicity of a test compound.

Group 34 claim(s) 30 and 35, drawn to a method for a diagnostic test for a condition or disease associated with the expression of NTRAN in a biological sample.

Group 35 claim(s) 44, drawn to a method of detecting a polypeptide.

Group 36 claim(s) 45, drawn to a method of purifying a polypeptide.

Group 37 claim(s) 46 and 48-55, drawn to a microarray.

Group 38 claim(s) 47, drawn to a method of generating an expression profile of a sample.

The inventions listed as Groups 1-38 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Group 1 recites the special technical feature of SEQ ID NO: 1, which is not required by any of the other groups.

Continuation of B. FIELDS SEARCHED Item 3:

WEST (PG Pubs, USPT, JPO, EPO, DERWENT); NCBI (PubMed); STN (CAPLUS, MEDLINE)

human neurotransmission-associated protein, SNAP, SNARE, synaptotagmin, Rab, WD Repeat, vesicle, neurotransmitter,

SEQ ID NO: 1, 14, 23, 36

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/40059

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 1-7, 9-10, 12-13, 17-18, 56, 69, 78, and 91 (each in part)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

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☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.